



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 181717

TO: Minh-Tam Davis
Location: REM-3A24&3C18
Art Unit: 1642
Thursday, March 09, 2006

Case Serial Number: 10/001469

From: Alex Waclawiw
Location: Biotech-Chem Library
Rem 1A71
Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

181717

From: Chan, Christina
Sent: Wednesday, March 08, 2006 2:25 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 10/001469

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

CRFE

-----Original Message-----

From: Davis, Minh-Tam
Sent: Wednesday, March 08, 2006 11:19 AM
To: Chan, Christina
Subject: Rush search request for 10/001469

Please search in commercial database, issued patent files, PGPUB and interference:
The protein of SEQ ID NO:2866
Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 3A24, MB 3C18
272-0830

4

Point of Contact:
Alexandra Wacławiw
Technical Info. Specialist

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 9, 2006, 08:21:49 , Search time 186 Seconds

(without alignments)
751.196 Million cell updates/sec

Title: US-10-001-469A-2866

Perfect score: 1622
Sequence: 1 MWVDPNGNSATRYFLIGL.....KEIRQRILRFVYATASRP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_21: *
1: geneeqp19808: *
2: geneeqp19908: *
3: geneeqp20008: *
4: geneeqp20018: *
5: geneeqp20028: *
6: geneeqp20038: *
7: geneeqp20048: *
8: geneeqp20058: *
9: geneeqp20068: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1622	100.0	318	7	AD109914 Optimised
2	1622	100.0	318	7	AD109880 101P3A11
3	1622	100.0	318	7	AD109871 101P3A11
4	1622	100.0	338	7	AD109912 Optimised
5	1619	99.8	318	3	AAV92365 G-protein
6	1619	99.8	318	4	AAW01306 P835P anti
7	1619	99.8	318	4	AAU63951 Human pro
8	1619	99.8	318	4	AAU63951 Human pro
9	1619	99.8	318	4	AAU63951 Human pro
10	1619	99.8	318	4	AAU63951 Human pro
11	1619	99.8	318	4	AAU63951 Human pro
12	1619	99.8	318	4	AAU63951 Human pro
13	1619	99.8	318	4	AAU63951 Human pro
14	1619	99.8	318	4	AAU63951 Human pro
15	1619	99.8	318	4	AAU63951 Human pro
16	1619	99.8	318	4	AAU63951 Human pro
17	1619	99.8	318	4	AAU63951 Human pro
18	1619	99.8	318	4	AAU63951 Human pro
19	1619	99.8	318	4	AAU63951 Human pro
20	1619	99.8	318	4	AAU63951 Human pro
21	1619	99.8	318	4	AAU63951 Human pro
22	1619	99.8	318	4	AAU63951 Human pro
23	1619	99.8	318	4	AAU63951 Human pro
24	1619	99.8	318	4	AAU63951 Human pro

25	1619	99.8	318	8	AD030402
26	1619	99.8	318	8	AD098144
27	1617	99.7	317	4	AA858002
28	1617	99.7	317	7	AD875619
29	1617	99.7	317	8	AD106545
30	1614	99.5	317	5	ABG61886
31	1614	99.5	317	7	AD862933
32	1614	99.5	317	7	ADN39555
33	1612	99.4	318	4	AB844535
34	1612	99.4	318	4	AB844535
35	1612	99.4	318	4	AB844535
36	1612	99.4	318	4	AB844535
37	1534	94.6	302	7	AD109903
38	1515	93.3	298	6	AD109904
39	1512	93.2	297	5	AB019532
40	1512	93.2	316	7	AD109908
41	1512	93.2	317	8	AD030422
42	1486	91.6	292	6	AD019531
43	1262	77.8	249	8	ADN58731
44	985	60.7	330	8	AD030425
45	979	60.4	315	4	AA671762
46	979	60.4	318	5	ABG68142
47	979	60.4	318	5	AAK39667
48	979	60.4	320	4	AAW01175
49	979	60.4	330	4	AAU69820
50	979	60.4	320	4	AA855135
51	979	60.4	320	4	AA855135
52	979	60.4	320	4	AA855135
53	979	60.4	320	4	AAU71711
54	979	60.4	320	4	AAU71711
55	979	60.4	320	4	AAU71711
56	979	60.4	320	4	AAU71711
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63	979	60.4	320	4	AAU71711
64	979	60.4	320	4	AAU71711
65	979	60.4	320	4	AAU71711
66	979	60.4	320	4	AAU71711
67	979	60.4	320	4	AAU71711
68	979	60.4	320	4	AAU71711
69	979	60.4	320	4	AAU71711
70	979	60.4	320	4	AAU71711
71	979	60.4	320	4	AAU71711
72	979	60.4	320	4	AAU71711
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85	979	60.4	320	4	AAU71711
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88	979	60.4	320	4	AAU71711
89	979	60.4	320	4	AAU71711
90	979	60.4	320	4	AAU71711
91	979	60.4	320	4	AAU71711
92	979	60.4	320	4	AAU71711
93	979	60.4	320	4	AAU71711
94	979	60.4	320	4	AAU71711
95	979	60.4	320	4	AAU71711
96	979	60.4	320	4	AAU71711
97	979	60.4	320	4	AAU71711

98 937.5 57.8 324 5 AAU85176 Aau85176 G-coupled
99 937.5 57.8 324 7 ADC86379 Adc86379 Human GPC
100 937.5 57.8 324 8 ADG83490 Adg83490 Human Olf

ALIGNMENTS

RESULT 1

AD109914
ID AD109914 standard; protein; 318 AA.

AC AD109914;

DT 22-APR-2004 (first entry)

DE Optimised 101P3A11v3 gene protein.

XX transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
KW stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.

XX Unidentified.

PN WO200292842-A2.

PD 21-NOV-2002.

PE 15-MAY-2002; 2002MO-US015520.

PR 15-MAY-2001; 2001US-0291118P.

PR 31-OCT-2001; 2001US-00001469.

PR 14-DEC-2001; 2001US-00017666.

XX (AGEN-) AGENSYS INC.

PI Jakobovits A, Faris M, Raitano AB, Morrison RK, Saffran D, Ge W,
PI Chailita-Bid PM;

DR WPI; 2003-129310/12.

PT New composition comprising 101P3A11-related protein, useful for
PT preventing or treating cancer e.g., stomach, cervix, uterus, rectum,
PT prostate, colon, kidney or breast cancer.

PS Claim 13; SEQ ID NO 5012; 327bp; English.

CC The invention relates to a novel composition comprising: a substance that
CC modulates the status of a protein comprising a sequence with a fully
CC defined 2466 or 3136 amino acid sequence given in the specification; or a
CC molecule that is immobilised by a protein comprising a sequence with a
CC fully defined 2466 or 3136 amino acids, where the status of a cell
CC expressing the protein is modulated. The invention further relates to: an
CC antibody; a non-human transgenic animal or hybridoma that produces the
CC antibody; a method of delivering a cytotoxic or diagnostic agent to a
CC cell that expresses the protein; a polynucleotide that encodes the
CC protein; a method for inhibiting the growth of cancer cells that express
CC the protein; a method for generating a mammalian immune response directed
CC to the protein; a method for detecting in a sample the presence of a 101P3A11
CC -related protein or polynucleotide; and a method for monitoring one or
CC more 101P3A11 gene products in a biological sample from a patient having
CC or suspected of having cancer. The novel composition has cytostatic
CC activity. The composition is useful for preventing or treating cancer
CC e.g., stomach, cervix, uterus, rectum, prostate, colon, kidney or breast
CC cancer. This sequence represents a 101P3A11 protein of the invention.

XX Sequence 318 AA;

Query Match 100.0%; Score 1622; DB 7; Length 318;

Best Local Similarity 100.0%; Pred. No. 1e-169;

Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFILGLPGLBEAQPWLAFLPCLSLYLIVAGNLTITIIYVTRTEHSLHE 60
|||||

DB 1 MMVDPNGNESSATYFILGLPGLBEAQPWLAFLPCLSLYLIVAGNLTITIIYVTRTEHSLHE 60
QY PMYFLICWLSGIDILISTNSMPKMLAIPWNSSTTIOPDACLLOIPALHSLSGMESTVLLA 120
|||
DB 61 PMYFLICWLSGIDILISTNSMPKMLAIPWNSSTTIOPDACLLOIPALHSLSGMESTVLLA 120
|||
QY 121 MAPDRYVAICHPLEBAATVLTLPRTYKIGVAAVVGAAALMAELPVFIKQLPFCRSNIISSH 180
DB 121 MAPDRYVAICHPLEBAATVLTLPRTYKIGVAAVVGAAALMAELPVFIKQLPFCRSNIISSH 180
QY 181 YCHODVWKLA CDDIRVVNVYGLVVISALIGLDSLLISFSYLLILKTVLGTTRBAQAAAF 240
DB 181 YCHODVWKLA CDDIRVVNVYGLVVISALIGLDSLLISFSYLLILKTVLGTTRBAQAAAF 240
QY 241 GTCVSHVCAVPIFYVPFGLSMVAFSGKRDSPLPVILANITLLVPPVLANPIYGVKTKE 300
DB 241 GTCVSHVCAVPIFYVPFGLSMVAFSGKRDSPLPVILANITLLVPPVLANPIYGVKTKE 300
QY 301 IRORIILRLFHVATHASBP 318
DB 301 IRORIILRLFHVATHASBP 318

RESULT 2

AD109880
ID AD109880 standard; protein; 318 AA.

AC AD109880;

DT 22-APR-2004 (first entry)

DE 101P3A11v1 gene protein.

XX transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
KW stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.

XX Unidentified.

PN WO200292842-A2.

PD 21-NOV-2002.

PE 15-MAY-2002; 2002MO-US015520.

PR 15-MAY-2001; 2001US-0291118P.

PR 31-OCT-2001; 2001US-00001469.

PR 14-DEC-2001; 2001US-00017666.

XX (AGEN-) AGENSYS INC.

PI Jakobovits A, Faris M, Raitano AB, Morrison RK, Saffran D, Ge W,
PI Chailita-Bid PM;

DR WPI; 2003-129310/12.

PT New composition comprising 101P3A11-related protein, useful for
PT preventing or treating cancer e.g., stomach, cervix, uterus, rectum,
PT prostate, colon, kidney or breast cancer.

PS Claim 13; SEQ ID NO 4096; 327bp; English.

CC The invention relates to a novel composition comprising: a substance that
CC modulates the status of a protein comprising a sequence with a fully
CC defined 2466 or 3136 amino acid sequence given in the specification; or a
CC molecule that is immobilised by a protein comprising a sequence with a
CC fully defined 2466 or 3136 amino acids, where the status of a cell
CC expressing the protein is modulated. The invention further relates to: an
CC antibody; a non-human transgenic animal or hybridoma that produces the
CC antibody; a method of delivering a cytotoxic or diagnostic agent to a
CC cell that expresses the protein; a polynucleotide that encodes the
CC protein; a method for inhibiting the growth of cancer cells that express
CC the protein; a method for generating a mammalian immune response directed
CC to the protein; a method for detecting in a sample the presence of a 101P3A11

CC -related protein or polynucleotide; and a method for monitoring one or
CC more 101P3A11 gene products in a biological sample from a patient having
CC or suspected of having cancer. The novel composition has cytostatic
CC activity. The composition is useful for preventing or treating cancer
CC e.g., stomach, cervix, uterus, rectum, prostate, colon, kidney or breast
CC cancer. This sequence represents a 101P3A11 protein of the invention.

XX Sequence 318 AA:

Query Match 100.0%; Score 1622; DB 7; Length 318;
Best Local Similarity 100.0%; Pred. No. 1e-169;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPMGNSSATYFLLIGLPGLEAQMFLAPLCSYLAVGNLTIIYVTEHSLHE 60
DB 1 MMVDPMGNSSATYFLLIGLPGLEAQMFLAPLCSYLAVGNLTIIYVTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSMRPMKLAIFWNSSTTIOPDACLQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSMRPMKLAIFWNSSTTIOPDACLQIFAIHSLSGMESTVLLA 120
QY 121 MAFDRYVALCHPLRHATVLTLPRTKIGVAAYVRGAAALMAPLPVFIKQLPFCRSNLSHS 180
DB 121 MAFDRYVALCHPLRHATVLTLPRTKIGVAAYVRGAAALMAPLPVFIKQLPFCRSNLSHS 180
QY 181 YCLHODVMKACDDIRNVVYGLIYIISAIGLDSLISFSYLLILKTVLGLTREBAQKAF 240
DB 181 YCLHODVMKACDDIRNVVYGLIYIISAIGLDSLISFSYLLILKTVLGLTREBAQKAF 240
QY 241 GTCVSHVCAVFIYVPFIGLSMVHRFSKRDSPLPYILANIYLLVPPVLPPIYGVYTKS 300
DB 241 GTCVSHVCAVFIYVPFIGLSMVHRFSKRDSPLPYILANIYLLVPPVLPPIYGVYTKS 300
QY 301 IRRRIILRLFRVATHASEP 318
DB 301 IRRRIILRLFRVATHASEP 318

RESULT 3

AD109871 AD109871 standard; protein; 318 AA.

XX AD109871;

DT 22-APR-2004 (first entry)

DB 101P3A11 protein region, amino acids 1-318.

XX transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
KW stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.

XX Unidentified.

XX WO200292842-A2.

XX 21-NOV-2002.

XX 15-MAY-2002; 2002MO-US015520.

XX 15-MAY-2001; 2001US-0291118P.

XX 31-OCT-2001; 2001US-0000146P.

XX 14-DEC-2001; 2001US-00017666.

XX (AGEN-) AGENSYS INC.

XX Jukobovics A, Paris M, Raitano AB, Morrison RK, Saffran D, Ge W;
PI Chailite-Eld PM;

XX WPI, 2003-129310/12.

XX New composition comprising 101P3A11-related protein, useful for
PT preventing or treating cancer e.g., stomach, cervix, uterus, rectum,
PT prostate, colon, kidney or breast cancer.

XX Claim 13; SEQ ID NO 4087; 327bp; English.

XX The invention relates to a novel composition comprising: a substance that
CC modulates the status of a protein comprising a sequence with a fully
CC defined 2466 or 3136 amino acid sequence given in the specification; or a
CC molecule that is immobilised by a protein comprising a sequence with a
CC fully defined 2466 or 3136 amino acids, where the status of a cell
CC expressing the protein is modulated. The invention further relates to: an
CC antibody; a non-human transgenic animal or hybridoma that produces the
CC antibody; a method of delivering a cytotoxic or diagnostic agent to a
CC cell that expresses the protein; a polynucleotide that encodes the
CC protein; a method for inhibiting the growth of cancer cells that express
CC the protein; a method for generating a mammalian immune response directed
CC to the protein; a method detecting in a sample the presence of a 101P3A11
CC -related protein or polynucleotide; and a method for monitoring one or
CC more 101P3A11 gene products in a biological sample from a patient having
CC or suspected of having cancer. The novel composition has cytostatic
CC activity. The composition is useful for preventing or treating cancer
CC e.g., stomach, cervix, uterus, rectum, prostate, colon, kidney or breast
CC cancer. This sequence represents a protein region of the 101P3A11 protein
CC of the invention.

XX Sequence 318 AA:

Query Match 100.0%; Score 1622; DB 7; Length 318;
Best Local Similarity 100.0%; Pred. No. 1e-169;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPMGNSSATYFLLIGLPGLEAQMFLAPLCSYLAVGNLTIIYVTEHSLHE 60
DB 1 MMVDPMGNSSATYFLLIGLPGLEAQMFLAPLCSYLAVGNLTIIYVTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSMRPMKLAIFWNSSTTIOPDACLQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSMRPMKLAIFWNSSTTIOPDACLQIFAIHSLSGMESTVLLA 120
QY 121 MAFDRYVALCHPLRHATVLTLPRTKIGVAAYVRGAAALMAPLPVFIKQLPFCRSNLSHS 180
DB 121 MAFDRYVALCHPLRHATVLTLPRTKIGVAAYVRGAAALMAPLPVFIKQLPFCRSNLSHS 180
QY 181 YCLHODVMKACDDIRNVVYGLIYIISAIGLDSLISFSYLLILKTVLGLTREBAQKAF 240
DB 181 YCLHODVMKACDDIRNVVYGLIYIISAIGLDSLISFSYLLILKTVLGLTREBAQKAF 240
QY 241 GTCVSHVCAVFIYVPFIGLSMVHRFSKRDSPLPYILANIYLLVPPVLPPIYGVYTKS 300
DB 241 GTCVSHVCAVFIYVPFIGLSMVHRFSKRDSPLPYILANIYLLVPPVLPPIYGVYTKS 300
QY 301 IRRRIILRLFRVATHASEP 318
DB 301 IRRRIILRLFRVATHASEP 318

RESULT 4

AD109912 AD109912 standard; protein; 338 AA.

XX AD109912;

DT 22-APR-2004 (first entry)

DB Optimised 101P3A11v1 gene protein.

XX transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
KW stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.

XX Unidentified.

XX WO200292842-A2.

XX 21-NOV-2002.

PF	15-MAY-2002; 2002MO-US015520.
PR	15-MAY-2001; 2001US-0291118P.
PR	31-OCT-2001; 2001US-00001469.
PR	14-DEC-2001; 2001US-00017666.
XX	(AGEN-) AGENSYS INC.
PA	Jakobovits A, Paris M, Raitano AB, Morrison RK, Saffran D, Ge W,
PI	Challita-Eld EM;
DR	WP1; 2003-129310/12.
XX	New composition comprising 10IP3A1-related protein, useful for
PT	preventing or treating cancer e.g., stomach, cervix, uterus, rectum,
PT	prostate, colon, kidney or breast cancer.
PS	Claim 13; SEQ ID NO 5010; 327bp; English.
XX	The invention relates to a novel composition comprising: a substance that
CC	modulates the status of a protein comprising a sequence with a fully
CC	defined 2466 or 3136 amino acid sequence given in the specification or a
CC	molecule that is immobilised by a protein comprising a sequence with a
CC	fully defined 2466 or 3136 amino acids, where the status of a cell
CC	expressing the protein is modulated. The invention further relates to: an
CC	antibody; a non-human transgenic animal or hybridoma that produces the
CC	antibody; a method of delivering a cytotoxic or diagnostic agent to a
CC	cell that expresses the protein; a polynucleotide that encodes the
CC	protein; a method for inhibiting the growth of cancer cells that express
CC	the protein; a method for generating a mammalian immune response directed
CC	to the protein; a method for detecting in a sample the presence of a 10IP3A1
CC	-related protein or polynucleotide; and a method for monitoring one or
CC	more 10IP3A1 gene products in a biological sample from a patient having
CC	activity. The composition is useful for preventing or treating cancer
CC	e.g., stomach, cervix, uterus, rectum, prostate, colon, kidney or breast
CC	cancer. This sequence represents a 10IP3A1 protein of the invention.
XX	Sequence 338 AA;
QY	Query Match 100.0%; Score 1622; DB 7; Length 338;
Db	Best Local Similarity 100.0%; Pred. No. 1,1e-169;
Matches	318; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 MMVDNGNESSATYFLLIGLPGLBEAQFWLAPPLCSLYIAVLGNLTIIIVRTEHSLHE 60
Db	1 MMVDNENGSSSATYFLTIGLPGLBEAQFWLAPPLCSLYIAVLGNLTIIIVRTERSHLR 60
QY	61 PMVITLCMLSGDILISTSMKMTALIFENSTTIOPDCLQIPIAHISLSGSESTVLLA 120
Db	61 PMVITLCMLSGDILISTSMKMTALIFENSTTIOPDCLQIPIAHISLSGSESTVLLA 120
QY	121 MAFDRTVAICHELRAHTVTLTPRVTKIGVAAVVRGAALAAPLVFPIKQLPFCRSNIISHS 180
Db	121 MAFDRTYAACHPLEARHTVTLTPRVTRKIGVAAVVRGAALMAAPLVFPIKQLPFCRSNIISHS 180
QY	131 YCHODDWKLACDDIRVVNVVGLIYISAIGDSLIISSYLLIKTVTGRLREAQAKP 240
Db	131 YCHODDWKLACDDIRVVNVVGLIYISAIGDSLIISSYLLIKTVTGRLREAQAKP 240
QY	181 YCHODDWKLACDDIRVVNVVGLIYISAIGDSLIISSYLLIKTVTGRLREAQAKP 240
Db	181 YCHODDWKLACDDIRVVNVVGLIYISAIGDSLIISSYLLIKTVTGRLREAQAKP 240
QY	241 GTGVSHVCAPVFIFYVPFIGLSNVHRPSKRSDPLPVILLANTYLVPVLANPVIYGVKTKE 300
Db	241 GTGVSHVCAPVFIFYVPFIGLSNVHRPSKRSDPLPVILLANTYLVPVLANPVIYGVKTKE 300
QY	301 IRQRILRLFHVATHASEP 318
Db	301 IRQRILRLFHVATHASEP 318
RESULT 5	
ID	AAY92365 standard; protein; 318 AA.
XX	

AC	AAV92365;		
DT	10-AUG-2000	(first entry)	
DE	G protein-coupled receptor protein 5.		
XX			
XX	GPCR-5; G protein-coupled receptor protein; antiparietic; antirheumatic		
KW	immunopressive; antiaesthetic; antianemic; antiatherosclerotic;		
KW	antichryoid; cyrostatic; haematocropic; dermatological; anti-inflammatory		
KW	antigout; thymomatous; haemostatic; virucide; hepatocropic; osteopathic		
KW	antiparasitic; immunostimulant.		
XX			
OS	Homo sapiens.		
XX			
FN	Key	location/Qualifiers	
FT	Peptide	1..26	
FT		/label= signal_peptide	
FT	Modified-site	8	
FT		/note= "potential glycosylation site"	
FT	Domain	34..52	
FT		/label= transmembrane	
FT	Modified-site	45	
FT		/note= "potential glycosylation site"	
FT	Modified-site	57	
FT		/note= "potential phosphorylation site"	
FT	Domain	62..83	
FT		/label= signature_sequence	
FT	Modified-site	70	
FT		/note= "G-protein coupled receptor"	
FT	Domain	91	
FT		/note= "potential phosphorylation site"	
FT	Modified-site	111	
FT		/note= "potential glycosylation site"	
FT	Domain	113..129	
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FT		/note= "G-protein coupled receptor"	
FT	Domain	202..225	
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FT	Modified-site	240..255	
FT		/note= "G-protein coupled receptor"	
FT	Domain	267	
FT		/label= signature_sequence	
FT	Modified-site	272	
FT		/note= "potential phosphorylation site"	
FT	Modified-site	272	
FT		/note= "potential phosphorylation site"	
XX			
XX	WO200020590-A2.		
XX			
XX	13-APR-2000.		
PD			
XX			
PE	06-OCT-1999;	99WD-US023317.	
XX			
XX	06-OCT-1998;	98US-00167219.	
XX	06-OCT-1998;	98US-0172211P.	
PR	11-MAY-1999;	99US-0133585P.	
XX			
XX			
PA	(INCY-) INCYTE PHARM INC.		
XX			
PI	Tang YT, Yue H, Lal P, Bandman O, Au-Young J, Reddy R,		
XX	Cotley NC, Guegler KJ, Gorgone GA, Baughn MR, Azimzal Y,		
XX	WPI; 2000-328934/28.		
DR	N-PSDB; AAA09351.		
XX			
PT	Novel human G-protein coupled receptor proteins used in the diagnosis,		
PT	treatment and prevention of nervous system disorders,		
PT	autoimmune/inflammatory disorders, and cell proliferative disorders such		
XX	as cancer.		

PS Claim 1; Page 71-72; 84pp; English.

CC This sequence encodes human G-protein coupled receptor protein (GCRP) 5.
 CC The GCRP polypeptides, polynucleotides, antibodies, antagonists and
 CC agonists may be administered to human patients for the diagnosis,
 CC treatment and prevention of nervous system disorders (e.g. epilepsy,
 CC stroke, neoplasms, Alzheimer's disease), autoimmune or inflammatory
 CC disorders, complications of cancer, hemodialysis and extracorporeal
 CC circulation, and cell proliferative disorders. They are also used to
 CC treat or prevent disorders associated with decreased or increased
 CC expression or activity of GCRP

XX Sequence 318 AA;

Query Match 99.8%; Score 1619; DB 3; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLAVGNLTIIYVRTESLHE 60
 DB 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLAVGNLTIIYVRTESLHE 60
 QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAHLSGMESTVLLA 120
 DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAHLSGMESTVLLA 120
 QY 121 MAPRYYAICHPLRHATVLTLPRTYKIGVAAVVGALMAPLPVFYIKQLPFCRSNIISHS 180
 DB 121 MAPRYYAICHPLRHATVLTLPRTYKIGVAAVVGALMAPLPVFYIKQLPFCRSNIISHS 180
 QY 181 YCHQDVWKLACDDIRNVVYGLVIISAIGLDSLISFSYLLTKTVLGLTREAOAKAF 240
 DB 181 YCHQDVWKLACDDIRNVVYGLVIISAIGLDSLISFSYLLTKTVLGLTREAOAKAF 240
 QY 241 GTCVSHVCAVFIYPVPFGLSMVHRFSKRSDPLPVILANIYLLVPVLPNIYVGVTKE 300
 DB 241 GTCVSHVCAVFIYPVPFGLSMVHRFSKRSDPLPVILANIYLLVPVLPNIYVGVTKE 300
 QY 301 IRQRILRLFHVATHASEP 318
 DB 301 IRQRILRLFHVATHASEP 318

RESULT 6

AA001306 ID AA001306 standard; protein; 318 AA.

XX AA001306;

XX 04-OCT-2001 (first entry)

XX P835P amino acid sequence.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;

KM cytoabatic; gene therapy; metastasis.

XX Homo sapiens.

XX WO200151633-A2.

XX 19-JUL-2001.

XX 16-JAN-2001; 2001WO-US001574.

XX 14-JAN-2000; 2000US-00483672.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocke SL, Jiang Y, Reed SG,
 PI Kalos MD, Fanger GR, Day CH, Retter MM, Stolk JA, Skelty YAM,
 PI Wang A, Meagher MJ;

XX WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
 PT monitoring and treating prostate cancer in a patient and for use in
 PT vaccines.

XX Claim 2; Page 534-535; 543pp; English.

CC The present invention describes polynucleotide sequences (I) which encode
 CC prostate-specific proteins (II). (I) and (II) have cytoabatic activity,
 CC and can be used in vaccine production and gene therapy. (I), (II),
 CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
 CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
 CC the antibodies are also used in the detection of cancer in a patient. The
 CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
 CC and (II) can be used in vaccines. The antibodies or (I) can be used for
 CC monitoring the progression of cancer in a patient. (I) and (II) can also
 CC be used to improve diagnostic and therapeutic methods for prostate
 CC cancer. They can indicate the level of metastasis as well as the prostate
 CC volume. AAH93357 to AAH93944 and AA001115 to AA001318 represent
 CC polynucleotide and amino acid sequences used in the exemplification of
 CC the present invention

XX Sequence 318 AA;

Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLAVGNLTIIYVRTESLHE 60
 DB 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLAVGNLTIIYVRTESLHE 60
 QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAHLSGMESTVLLA 120
 DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAHLSGMESTVLLA 120
 QY 121 MAPRYYAICHPLRHATVLTLPRTYKIGVAAVVGALMAPLPVFYIKQLPFCRSNIISHS 180
 DB 121 MAPRYYAICHPLRHATVLTLPRTYKIGVAAVVGALMAPLPVFYIKQLPFCRSNIISHS 180
 QY 181 YCHQDVWKLACDDIRNVVYGLVIISAIGLDSLISFSYLLTKTVLGLTREAOAKAF 240
 DB 181 YCHQDVWKLACDDIRNVVYGLVIISAIGLDSLISFSYLLTKTVLGLTREAOAKAF 240
 QY 241 GTCVSHVCAVFIYPVPFGLSMVHRFSKRSDPLPVILANIYLLVPVLPNIYVGVTKE 300
 DB 241 GTCVSHVCAVFIYPVPFGLSMVHRFSKRSDPLPVILANIYLLVPVLPNIYVGVTKE 300
 QY 301 IRQRILRLFHVATHASEP 318
 DB 301 IRQRILRLFHVATHASEP 318

RESULT 7

AA069951 ID AA069951 standard; protein; 318 AA.

XX AA069951;

XX 30-JAN-2002 (first entry)

XX Human prostate cDNA encoded protein #85.

KM Human; prostate cancer; cytoabatic; immunostimulant; tumour; immunogen.

XX Homo sapiens.

XX WO200173032-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US009919.

KM anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity;
 KM anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
 KM asthma; Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KM infection; human immunodeficiency virus; HIV.
 OS Homo sapiens.
 XX
 PN WO200174904-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US010241.
 XX
 PR 31-MAR-2000; 2000US-0193664P.
 PR 05-APR-2000; 2000US-0194614P.
 PR 06-APR-2000; 2000US-0195063P.
 PR 06-APR-2000; 2000US-0195066P.
 PR 06-APR-2000; 2000US-0195067P.
 PR 06-APR-2000; 2000US-0195068P.
 PR 06-APR-2000; 2000US-0195069P.
 PR 06-APR-2000; 2000US-0195070P.
 PR 06-APR-2000; 2000US-019510P.
 PR 21-JUL-2000; 2000US-0219855P.
 PR 27-JUL-2000; 2000US-0221284P.
 PR 28-JUL-2000; 2000US-0221325P.
 PR 11-AUG-2000; 2000US-0234588P.
 PR 11-OCT-2000; 2000US-0239613P.
 PR 18-JAN-2001; 2001US-0262508P.
 PR 23-JAN-2001; 2001US-0263433P.
 PR 23-JAN-2001; 2001US-0263604P.
 PR 30-JAN-2001; 2001US-0265161P.
 PR 29-MAR-2001; 2001US-00823172.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Majumder K, Vernet CM, Caeman SJ, Wolenc AR, Spaderna SK;
 PI Pedigaru M, Mishnu VS, Tchervet VT, Spytek KA, Li L, Baumgartner JC;
 PI Gusev VY;
 DR N-PSDB; ABA81542.
 XX
 DR WPI; 2001-639351/73.
 XX
 PT New human G-protein coupled receptor X, GPCR, polypeptide useful in
 PT treatment or prevention of GPCR associated disorders e.g. cardiomyopathy
 PT or atherosclerosis, and to screen for antagonists and agonists useful
 PT therapeutically.
 XX
 PS Claim 1; Page 55; 157p; English.
 XX
 CC The invention relates to nucleic acid sequences (ABA61529-ABA81552) that
 CC encode G-coupled protein-receptor related polypeptides (ABA44522-
 CC ABA44543). The isolated polypeptide having a sequence differing by no
 CC more than 15 % of amino acid residues from one of 22 amino acid sequences
 CC (or mature forms of the sequences), fully defined in the specification
 CC and corresponding to human G-protein coupled receptor X (GPCRX)
 CC polypeptides. The polypeptides have potential cardiac,
 CC antiatherosclerotic, anabolic, cytostatic and antiviral activity. The
 CC polypeptides can be administered therapeutically, especially using gene
 CC therapy and expressing the encoding DNA in vivo, to treat or prevent
 CC GPCR-associated disorders, especially in humans. For example, they can
 CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
 CC related to signal processing and metabolic pathway modulation (e.g. obesity,
 CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
 CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease), immune disorders,
 CC hematopoietic disorders, developmental diseases, neurological disorders,
 CC bacterial, fungal, protozoal and viral infections (e.g. with human
 CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
 CC to determine the presence of or predisposition to a disease associated
 CC with altered levels of the polypeptide expression in mammals (especially humans) by
 CC detecting alterations in polypeptide expression levels relative to
 CC control samples. They are useful to identify agents binding polypeptide
 CC (e.g. cellular receptors or downstream effectors) and/or agents

CC modulating cellular polypeptide expression or activity, useful as
 CC antagonists and agonists in disease treatment
 XX
 SO Sequence 318 AA;
 Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. NO. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVDPNNGESSATYFLLIGLGLBEAQFWLAPLCSLYLTAAGNLTIIYVRESHLH 60
 DB 1 MMVDPNNGESSATYFLLIGLGLBEAQFWLAPLCSLYLTAAGNLTIIYVRESHLH 60
 QY 61 PMYIFLCMLSGIDILISTSMPPKMLAFWENSTTIQPDACILQIFAIHLSGMESTVLLA 120
 DB 61 PMYIFLCMLSGIDILISTSMPPKMLAFWENSTTIQPDACILQIFAIHLSGMESTVLLA 120
 QY 121 MAPDRYVAICHPLRHATVTLTPRVTKIGVAAVVRGAALMAPLPVFIKQLPCCRNIISHS 180
 DB 121 MAPDRYVAICHPLRHATVTLTPRVTKIGVAAVVRGAALMAPLPVFIKQLPCCRNIISHS 180
 QY 121 MAPDRYVAICHPLRHATVTLTPRVTKIGVAAVVRGAALMAPLPVFIKQLPCCRNIISHS 180
 DB 181 YCLHODVMKACDIDIRNNVYGLIIVISATGLDLSISFYLITLKTVLGLTRBAQAKAF 240
 QY 181 YCLHODVMKACDIDIRNNVYGLIIVISATGLDLSISFYLITLKTVLGLTRBAQAKAF 240
 DB 241 GTCVSHVCAVFIFFVPEIGLSMYRFSKRDSPLPVILANIYLLVPVLPVIYGVGVTKE 300
 QY 241 GTCVSHVCAVFIFFVPEIGLSMYRFSKRDSPLPVILANIYLLVPVLPVIYGVGVTKE 300
 DB 301 IRRRIIRLPHVATHASEP 318
 QY 301 IRRRIIRLPHVATHASEP 318
 DB 301 IRRRIIRLPHVATHASEP 318
 RESULT 11
 AB071842
 ID AB071842 standard; protein; 318 AA.
 XX
 AC AB071842;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Prostate cancer associated protein #66.
 XX
 KM Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KM immunogen; cancer; prostate specific antigen; PSA;
 KM prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KM PSA.
 XX
 OS Homo sapiens.
 XX
 XX US2002192763-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 29-JUN-2001; 2001US-00895793.
 XX
 PR 04-OCT-1999; 99US-0157455P.
 PR 04-OCT-2000; 2000US-00679272.
 PR 28-MAR-2001; 2001US-00822827.
 XX
 PA (XUJ)/ XU J.
 PA (DILL)/ DILLON D C.
 PA (MITC)/ MITCHAM J L.
 PA (HARK)/ HARTLOCKER S L.
 PA (JIAN)/ JIANG Y.
 PA (KALO)/ KALOS M D.
 PA (FANG)/ FANGER G R.
 PA (RETT)/ RETTER M W.
 PA (STOL)/ STOLK J A.
 PA (DAYC)/ DAY C H.
 PA (VEDV)/ VEDVICK T S.
 PA (CART)/ CARTER D.

PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEL/) SKELLY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOU/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.
 PI Xu J, Dillon DC, Mitcham JT, Harlocker SL, Jiang Y, Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D, Li SX, Wang A, Skeily YAM, Hepler WF, Henderson RA, Hural J, McNeill PD, Houghton RL, Y De BassolsCV, Foy TM,
 PI WPI; 2001-245062/25.
 DR
 PT Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.
 PT
 XX Example 15; SEQ ID NO 920; 85bp; English.
 PS
 XX The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not CC defined in the specification, or sequences having at least 70 or 90 % CC sequence identity to any one of the 4 nucleotide sequences not defined CC in the specification. The fusion protein, composition and methods are CC useful for diagnosing, preventing and/or treating cancer, particularly CC prostate cancer. The proteins are useful as markers to indicate the CC presence or absence of cancer. This is the amino acid sequence of a CC prostate cancer therapy associated protein. Note: The sequence data for CC this patent did not form part of the printed specification, but was CC obtained in electronic format directly from the US patent office at CC seqdata.uspto.gov/sequence.html?docid=US20020192763
 XX
 XX Sequence 318 AA;
 SO
 Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVDPNNESSATYFILIGLPGLEAQMFLAFPLCSLYLAVGNLTIIYVTRHSLHE 60
 DB 1 MMVDPNNESSATYFILIGLPGLEAQMFLAFPLCSLYLAVGNLTIIYVTRHSLHE 60
 QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
 DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
 QY 121 MAFDRVYAICHPRBHATVTLTPRVTKIGVAAVVRGALMALPLPVFIKQLPFCRSNIIISHS 180
 DB 121 MAFDRVYAICHPRBHATVTLTPRVTKIGVAAVVRGALMALPLPVFIKQLPFCRSNIIISHS 180
 QY 181 YCHHODVMKLAACDIRNVVYGLIIVISAIGLDSLISFSYLLIKTKVLGITREAOAKAF 240
 DB 181 YCHHODVMKLAACDIRNVVYGLIIVISAIGLDSLISFSYLLIKTKVLGITREAOAKAF 240
 QY 241 GTCVSHVCAVFIFFVPPIGLSMVRFSKRSDSPPLVILANITYLLVPPVLANPIYGVATKE 300
 DB 241 GTCVSHVCAVFIFFVPPIGLSMVRFSKRSDSPPLVILANITYLLVPPVLANPIYGVATKE 300
 QY 301 IRORIILRFVATRASAP 318
 DB 301 IRORIILRFVATRASAP 318
 RESULT 12
 ID AAU24561 standard; protein; 318 AA.
 XX
 AC AAU24561;

XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human olfactory receptor AOLF48.
 XX
 KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant; food additive; cosmetic; fragrance; pharmaceutical additive.
 XX
 OS Homo sapiens.
 XX
 PN WO200168805-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001KO-US007771.
 XX
 PR 13-MAR-2000; 2000US-0188914P.
 PR 24-MAR-2000; 2000US-0192033P.
 PR 12-APR-2000; 2000US-0198474P.
 PR 24-APR-2000; 2000US-0199335P.
 PR 26-MAY-2000; 2000US-0207702P.
 PR 23-JUN-2000; 2000US-0213849P.
 PR 16-AUG-2000; 2000US-0226534P.
 PR 07-SEP-2000; 2000US-0230732P.
 PR 07-FEB-2001; 2001US-0266862P.
 XX
 FA (SENO-) SENOMTX INC.
 XX
 PI Zozulya S;
 XX
 DR WPI; 2001-570867/64.
 DR N-PSDB; AAS42254.
 XX
 PT Nucleic acids encoding human olfactory G protein-coupled receptors, where the compounds can be used in the food, pharmaceutical and cosmetic industries to customise odors.
 PT
 XX
 XX Claim 60; Page 103-104; 319pp; English.
 PS
 XX The invention relates to nucleic acids encoding human olfactory CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's CC specifically recognise molecules, odourants, that elicit specific CC olfactory sensation. The human olfactory receptors and polynucleotides CC encoding them are useful for screening a library of chemical compounds CC for compounds that are involved in olfactory sensation. Modulators of CC their activity are useful for pharmacological and genetic modulation of CC olfactory signalling pathways. Therefore, they can be used in the food, CC pharmaceutical and cosmetic industries to customise odours and CC fragrances. The present sequence is a human olfactory receptor of the CC invention
 CC
 XX
 SO Sequence 318 AA;
 Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVDPNNESSATYFILIGLPGLEAQMFLAFPLCSLYLAVGNLTIIYVTRHSLHE 60
 DB 1 MMVDPNNESSATYFILIGLPGLEAQMFLAFPLCSLYLAVGNLTIIYVTRHSLHE 60
 QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
 DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
 QY 121 MAFDRVYAICHPRBHATVTLTPRVTKIGVAAVVRGALMALPLPVFIKQLPFCRSNIIISHS 180
 DB 121 MAFDRVYAICHPRBHATVTLTPRVTKIGVAAVVRGALMALPLPVFIKQLPFCRSNIIISHS 180
 QY 181 YCHHODVMKLAACDIRNVVYGLIIVISAIGLDSLISFSYLLIKTKVLGITREAOAKAF 240
 DB 181 YCHHODVMKLAACDIRNVVYGLIIVISAIGLDSLISFSYLLIKTKVLGITREAOAKAF 240

QY 241 GTCVSHVCAVFIYVPPFGLSMVHRFSKRDSPVLILANITYLLVPPVLPNIYGVGVTKE 300
DB 241 GTCVSHVCAVFIYVPPFGLSMVHRFSKRDSPVLILANITYLLVPPVLPNIYGVGVTKE 300
QY 301 IRQRILRLFHVATASEP 318
DB 301 IRQRILRLFHVATASEP 318
RESULT 13
ABP95411
ID ABB95411 standard; protein, 318 AA.
AC ABB95411;
XX 19-JUL-2002 (first entry)
XX Human P835P protein SEQ ID NO 920.
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy.
XX Homo sapiens.
XX OS
XX US2002022248-A1.
XX 21-FEB-2002.
XX 12-JAN-2001; 2001US-00759143.
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 10-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 10-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
DR WPI: 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
PS Claim 2; SEQ ID NO 920; 87bp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a
CC protein described in the invention
XX
SQ Sequence 318 AA;
Query Match 99.8%; Score 1619; DB 5; Length 318;
Best Local Similarity 99.7%; Pred. No. 2.2e-169;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMYDPNGNBSATYFIILGPGLEAOFWLAFLCSYLLAVLGNLTITTYVTRHSILHE 60
DB 1 MMYDPNGNBSATYFIILGPGLEAOFWLAFLCSYLLAVLGNLTITTYVTRHSILHE 60
QY 61 PMYFELCMLSGIDLITSSMPKMLAFWFNSTTIOPDACLQIFAHISISGMESTVLLA 120
DB 61 PMYFELCMLSGIDLITSSMPKMLAFWFNSTTIOPDACLQIFAHISISGMESTVLLA 120
QY 121 MAFDRYVAICHPLRHATVLTLPRTKIGVAAVVGAAALMPLPVFIKOLPFCRSNITLSHS 180
DB 121 MAFDRYVAICHPLRHATVLTLPRTKIGVAAVVGAAALMPLPVFIKOLPFCRSNITLSHS 180
QY 181 YCHLDQWKLACDDIRVNVVYGLIIVISAIIGDLSLISFSTYLLIKTVLGLTRBAQAKAF 240
DB 181 YCHLDQWKLACDDIRVNVVYGLIIVISAIIGDLSLISFSTYLLIKTVLGLTRBAQAKAF 240
QY 241 GTCVSHVCAVFIYVPPFGLSMVHRFSKRDSPVLILANITYLLVPPVLPNIYGVGVTKE 300
DB 241 GTCVSHVCAVFIYVPPFGLSMVHRFSKRDSPVLILANITYLLVPPVLPNIYGVGVTKE 300
QY 301 IRQRILRLFHVATASEP 318
DB 301 IRQRILRLFHVATASEP 318
RESULT 14
ABP95674
ID ABB95674 standard; protein, 318 AA.
AC ABB95674;
XX 06-MAR-2003 (first entry)
XX Human GPCR polypeptide SEQ ID NO 158.
XX
XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; receptor.
XX Homo sapiens.
XX OS
XX WO200216548-A2.
XX 28-FEB-2002.
XX 30-JUL-2001; 2001WO-1B001446.
XX 04-AUG-2000; 2000JP-00237818.
XX 13-FEB-2001; 2001JP-00034434.
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PI Haga T, Takeda S, Mitaku S;
 XX WPI; 2002-304118/34.
 DR N-PSDB; AB242948.
 XX Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development.
 XX Claim 10; SEQ ID NO 158; 97pp + Sequence listing; Japanese.
 XX
 CC The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-
 CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
 CC domains with 250-1000 amino acid residues to give a gene homologous with
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for
 CC studying in vivo signal transduction mechanism and identifying targets
 CC for drug development e.g. based on olfactory and gustatory receptors in
 CC form of agonists and antagonists by screening intrinsic and extrinsic
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance
 CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 318 AA;
 Query Match 99.8%; Score 1619; DB 5; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMYDPNGNESSATYFIIIGLPGLEBAQFMFLAPLCSLYLAVNGNLTIIYVTRTHSLH 60
 DB 1 MMYDPNGNESSATYFIIIGLPGLEBAQFMFLAPLCSLYLAVNGNLTIIYVTRTHSLH 60
 QY 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIGDACLQIFAIHSLSGNESTVLLA 120
 DB 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIGDACLQIFAIHSLSGNESTVLLA 120
 QY 121 MADDRVYALCHPRHATVTLPRVTYKIGVAAVVRGALMAPLPVFYKQLPFCNSNIISHS 180
 DB 121 MADDRVYALCHPRHATVTLPRVTYKIGVAAVVRGALMAPLPVFYKQLPFCNSNIISHS 180
 QY 181 YCHADQVAKLACDDIRNVVYGLIIVISAIGLSLISFSYLLIKTVLGLTREAOAKAF 240
 DB 181 YCHADQVAKLACDDIRNVVYGLIIVISAIGLSLISFSYLLIKTVLGLTREAOAKAF 240
 QY 241 GTCVSHCAVFIFFVYFPIGLSMVHRFSKRDSPLPVIANIYLLVPPVLPPIYGVYTKS 300
 DB 241 GTCVSHCAVFIFFVYFPIGLSMVHRFSKRDSPLPVIANIYLLVPPVLPPIYGVYTKS 300
 QY 301 IRRQILRLFRVATHASRP 318
 DB 301 IRRQILRLFRVATHASRP 318
 ID AAU95746 standard; protein; 318 AA.
 AC AAU95746;
 XX
 DT 02-JUL-2002 (first entry)
 XX Human olfactory and pheromone G protein-coupled receptor #233.
 XX Human; olfactory and pheromone G protein coupled; receptor; GPCR;
 KM transquillizer; antidepressant; neuroleptic; endocrine; anabolic;
 KM anorectic; taste; fragrance; food additive; cosmetic; cell migration;
 KM sterility; psychotic disorder; neurological disorder; anxiety;
 KM schizophrenia; manic depression; depression; axonal growth;
 KM menstrual cycle; appetite sexual motivation; sexual attraction;
 XX aggression.
 XX

OS Homo sapiens.
 XX
 PN W0200224726-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 21-SEP-2001; 2001WO-BE000162.
 XX
 PR 22-SEP-2000; 2000EP-00870211.
 XX
 PA (CHEM-) CHEMCOM SA.
 PI Velthuis A;
 XX
 DR WPI; 2002-330013/36.
 DR N-PSDB; ABK68633.
 XX
 PT Novel pheromone G-protein coupled receptor and receptor-derived agonists,
 PT antagonists or inhibitors useful in food or cosmetic products or in the
 PT treatment or prevention of neurological disorders such as anxiety and
 PT schizophrenia.
 XX
 PS Disclosure; Page 710-711; 833pp; English.
 XX
 CC The invention relates to olfactory and Pheromone G-protein coupled
 CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
 CC portion and its encoding polynucleotide. Also included are an agonist,
 CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector
 CC comprising the polynucleotide, a cell transformed by the vector, a non-
 CC human mammal comprising a partial or total deletion of the polynucleotide
 CC encoding the receptor and screening (detection and possibly, recovering)
 CC of compounds which are known or not known to be agonist, antagonists or
 CC inhibitors of natural compounds to the GPCR. The receptor-derived
 CC agonists, antagonists, inhibitors or compounds are used as an
 CC improvement, elimination or substitution of an existing taste and/or a
 CC fragrance of (or in) the food and/or cosmetic products. They can also be
 CC used in the preparation of medicament in the treatment and/or prevention
 CC of a mammalian disorder, such as cell migration, sterility, psychotic and
 CC neurological disorders, including anxiety, schizophrenia, manic
 CC depression, depression, for promoting axonal growth, nerve cell
 CC connection and nerve regeneration for modulating male and female
 CC endocrine functions, hormone production and the menstrual cycle, for the
 CC prevention or the treatment by stimulation of several mammalian
 CC behaviours, such as stimulation or suppression of appetite, sexual
 CC motivation, sexual attraction, aggression and for promoting or
 CC suppressing chemical communication between organisms. The present
 CC sequence is a human olfactory and pheromone GPCR protein sequence
 XX
 SQ Sequence 318 AA;
 Query Match 99.8%; Score 1619; DB 5; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMYDPNGNESSATYFIIIGLPGLEBAQFMFLAPLCSLYLAVNGNLTIIYVTRTHSLH 60
 DB 1 MMYDPNGNESSATYFIIIGLPGLEBAQFMFLAPLCSLYLAVNGNLTIIYVTRTHSLH 60
 QY 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIGDACLQIFAIHSLSGNESTVLLA 120
 DB 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTTIGDACLQIFAIHSLSGNESTVLLA 120
 QY 121 MADDRVYALCHPRHATVTLPRVTYKIGVAAVVRGALMAPLPVFYKQLPFCNSNIISHS 180
 DB 121 MADDRVYALCHPRHATVTLPRVTYKIGVAAVVRGALMAPLPVFYKQLPFCNSNIISHS 180
 QY 181 YCHADQVAKLACDDIRNVVYGLIIVISAIGLSLISFSYLLIKTVLGLTREAOAKAF 240
 DB 181 YCHADQVAKLACDDIRNVVYGLIIVISAIGLSLISFSYLLIKTVLGLTREAOAKAF 240
 QY 241 GTCVSHCAVFIFFVYFPIGLSMVHRFSKRDSPLPVIANIYLLVPPVLPPIYGVYTKS 300
 DB 241 GTCVSHCAVFIFFVYFPIGLSMVHRFSKRDSPLPVIANIYLLVPPVLPPIYGVYTKS 300

QY 301 IRORIIRLFHVATTHASEP 318
DB 301 IRORIIRLFHVATTHASEP 318

RESULT 16
AAU85181
ID AAU85181 standard; protein; 318 AA.

AC AAU85181;
XX
DT 08-MAY-2002 (first entry)
XX
DE G-coupled olfactory receptor #42.

XX Human; olfactory G-coupled receptor; sensory perception of odourant;
KM odour composition; taste composition.
XX
OS Homo sapiens.
XX
PN W0200198536-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020122.
XX
PR 22-JUN-2000; 2000US-0213812P.
XX
PR 13-MAR-2001; 2001US-00804291.
XX
PA (SENO-) SENOMYX INC.
XX
PI Zozulya S, Stryer L;
XX WPI; 2002-083330/11.
XX
DR N-PSDB; ABK37540.
XX
PT Representing sensory perception of one or more odourants for the
PT identification and design of tastes and odors comprises providing a
PT representative group of n olfactory receptors.
XX
XX
XX Claim 1; Page 77; 182pp; English.

CC The invention relates to a method of representing sensory perception of
CC one or more odourants. The method comprises: (a) providing a
CC representative class of n olfactory receptors or ligand binding domains
CC (LBD) of these receptors; (b) measuring values X1 to Xn representative of
CC at least one activity of one or more odourants selected from: (i) binding
CC one or more odourants to the LBD of at least one of the n olfactory
CC receptors; (ii) activating at least one of the n olfactory receptors with
CC the one or more odourants; and (iii) blocking at least one of the n
CC olfactory receptors with the one or more odourants; and (c) generating a
CC representation of sensory perception from the values X1 to Xn. The
CC representation of the sensory perception of odourants is useful for the
CC design and formulation of odour and taste compositions. AAU85140-AAU85393
CC represent human olfactory G-coupled receptor amino acid sequences of the
CC invention
XX
XX
SQ Sequence 318 AA;

Query Match 99.8%; Score 1619; DB 5; Length 318;
Best Local Similarity 99.7%; Pred. No. 2.2e-169;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAVDPNNGESSATTFFILIGLPGLEBAQFWLAPPLCSLYLIANLGLTIIYVTRHSHAE 60
DB 1 MAAVDPNNGESSATTFFILIGLPGLEBAQFWLAPPLCSLYLIANLGLTIIYVTRHSHAE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWPNSTTIQDPACCLLOTPAHISLSGMSSTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWPNSTTIQDPACCLLOTPAHISLSGMSSTVLLA 120
QY 121 MAFDRYVAICHPLRHATVLTLPVTYKIGVAAVRGALMALPVPFIKQLPFCRSNLSHS 180

DB 121 MAFDRYVAICHPLRHATVLTLPVTYKIGVAAVRGALMALPVPFIKQLPFCRSNLSHS 180
QY 181 YCHADQPMKACCDIRNNVYGLIVITISATGDSLLISPEYLLIKTVLGLTTRAAQKAF 240
DB 181 YCHADQPMKACCDIRNNVYGLIVITISATGDSLLISPEYLLIKTVLGLTTRAAQKAF 240
QY 241 GTCVSHVCAVFIFFVPPIGLSMVRFSKRSDSPPLVILANIYLLVPPVLPNIYGVKTKS 300
DB 241 GTCVSHVCAVFIFFVPPIGLSMVRFSKRSDSPPLVILANIYLLVPPVLPNIYGVKTKS 300
QY 301 IRORIIRLFHVATTHASEP 318
DB 301 IRORIIRLFHVATTHASEP 318

RESULT 17
ABO19491
ID ABO19491 standard; protein; 318 AA.

XX
AC ABO19491;
XX
DT 28-AUG-2003 (first entry)
XX
DE Human G protein-coupled receptor HGPBMY4.
XX
XX Human; receptor; G protein-coupled receptor; HGPBMY4; prostatitis;
KM Chagas's disease; post-inflammatory pseudotumour; infection; asthma;
KM benign prostatic hyperplasia; cancer; anorexia; Parkinson's disease;
KM acute heart failure; hypotension; hypertension; osteoporosis; ulcer;
KM neurological disorder; AIDS; allergy; anaemia; atherosclerosis;
KM Crohn's disease; atopic dermatitis; diabetes mellitus; emphysema;
KM Grave's disease; lupus erythematosus; multiple sclerosis; vaccine;
KM myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis;
KM rheumatoid arthritis; psoriasis; Sjogren's syndrome; truma;
KM autoimmune thyroiditis; Alzheimer's disease; amnesia; bipolar disorder;
KM amyotrophic lateral sclerosis; schizophrenia; Tourette's disorder.
XX
XX Homo sapiens.
XX
XX US2003022237-A1.
XX
XX
XX 30-JAN-2003.
XX
XX 26-SEP-2001; 2001US-0096459.
XX
XX 27-SEP-2000; 2000US-0235833P.
XX
XX 16-JAN-2001; 2001US-0261776P.
XX
XX 13-JUN-2001; 2001US-0305351P.
XX
XX 17-AUG-2001; 2001US-0313202P.

PA (FEDER/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAWK/) HAWKEN D R.
PA (CACACE/) CACACE A.
PA (BARB/) BARBER L.
PA (KORN/) KORNACKER M G.

XX
XX Feder JN, Mintier G, Ramanathan CS, Hawken DR, Cacace A;
PI Barber L, Kornacker MG;
XX
XX WPI; 2003-492001/46.
XX
XX N-PSDB; ACD29000.

PT New human G-protein coupled receptor polypeptide, HGPBMY4, expressed
PT highly in prostate, colon and lung, useful for treating/preventing
PT cancer, immune, neurological, cardiovascular, colon and lung-related
PT disorders.
XX
XX Claim 11; Fig 2; 74pp, English.

CC The invention relates to a new isolated G protein-coupled receptor

CC polypeptide HGPBMY4, comprising a sequence at least 95% identical to the
 CC protein appearing as ABO13491, or the encoded sequence of ATCC PTA-2682,
 CC the polypeptide fragment, domain, epitope, allelic variant, species
 CC homologue or a polypeptide corresponding to amino acids 2-318 of
 CC HGPBMY4. Also included are the nucleic acid encoding HGPBMY4 (and its
 CC fragment, allelic variant and complements), a recombinant vector
 CC comprising the nucleic acid, a recombinant host cell comprising the
 CC nucleic acid (and expressing HGPBMY4), an anti-HGPBMY4 antibody, a gene
 CC corresponding to the HGPBMY4 cDNA sequence, a compound that modulates
 CC the biological activity of human HGPBMY4, a cell comprising NFAT/CRE
 CC (not defined) and HGPBMY4 and a cell comprising NFAT G alpha 15 and
 CC HGPBMY4. HGPBMY4 or nucleic acid is useful for preventing, treating, or
 CC ameliorating e.g. a disease, disorder, or condition related to colon,
 CC breast, ovaries, or immune system (e.g. prostatitis, Chagas' disease,
 CC post-inflammatory pseudotumour, benign prostatic hyperplasia, bacterial,
 CC fungal, protozoan, and viral infections, particularly HIV-1 and HIV-2,
 CC cancers, anorexia, asthma, Parkinson's disease, acute heart failure,
 CC hypotension, hypertension, urinary retention, osteoporosis, ulcer,
 CC neurological disorders, AIDS, Addison's disease, allergies, anaemia,
 CC atherosclerosis, bronchitis, Crohn's disease, ulcerative colitis, atopic
 CC dermatitis, diabetes mellitus, emphysema, glomerulonephritis, gout,
 CC Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia
 CC gravis, myocardial or pericardial inflammation, osteoarthritis,
 CC osteoporosis, pancreatitis, rheumatoid arthritis, psoriasis, scleroderma,
 CC Sjogren's syndrome, and autoimmune thyroiditis, complications of cancer,
 CC haemodialysis and extracorporeal circulation, trauma, Alzheimer's
 CC disease, amnesia, amyotrophic lateral sclerosis, bipolar disorder,
 CC schizophrenia and Tourette's disorder. HGPBMY4 is also useful as a
 CC vaccine. HGPBMY4 is useful for identifying binding partners and
 CC ant/agonists. The present sequence represents HGPBMY4

XX Sequence 318 AA:

Query Match 99.8%; Score 1619; DB 6; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFLCSYLIVAGNLTIIYIVRTESLHE 60
 DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFLCSYLIVAGNLTIIYIVRTESLHE 60
 QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAIHSLSGMESTVLLA 120
 DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAIHSLSGMESTVLLA 120
 QY 121 MAFDRVVAICHPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIRKQLPFCRSNIIISHS 180
 DB 121 MAFDRVVAICHPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIRKQLPFCRSNIIISHS 180
 QY 181 YCLHODVMKLAACDDIRVVNVYGLIIVISAIGLDSLISFSYLLIKTVLGLTRBAQAKAF 240
 DB 181 YCLHODVMKLAACDDIRVVNVYGLIIVISAIGLDSLISFSYLLIKTVLGLTRBAQAKAF 240
 QY 241 GTCVSHCAVFIIVPPIGISMVHRFSKRDSPLPVLIANIYLLVPPVLPVIYGVYTKK 300
 DB 241 GTCVSHCAVFIIVPPIGISMVHRFSKRDSPLPVLIANIYLLVPPVLPVIYGVYTKK 300
 QY 301 IRORIILRFVATTHASEP 318
 DB 301 IRORIILRFVATTHASEP 318

RESULT 18

ABR54523 ID ABR54523 standard; protein; 318 AA.

XX ABR54523;

XX AC ABR54523;

XX DT 28-AUG-2003 (first entry)

XX XX Prostate tumour specific protein SEQ ID 920.
 XX XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;

KM Immune response; prostate cancer.

XX Homo sapiens.

XX WO200289747-A2.

XX 14-NOV-2002.

XX 09-MAY-2002; 2002WO-US014753.

XX 09-MAY-2001; 2001US-00852911.

XX 29-JUN-2001; 2001US-00895814.

XX 10-DEC-2001; 2001US-00012896.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kaloe MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skelky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De Basolsac, Foy TM, Watanabe Y;
 PI Deng T;

XX WPI; 2003-167130/16.

XX New prostate-specific proteins and genes, useful in gene therapy,
 PT particularly for stimulating an immune response in a patient, or treating
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer
 PT in a patient.

XX Example 15; Page 638; 691pp; English.

XX The present invention relates to novel prostate-specific proteins (PSP)

XX and their coding sequences. The PSPs and their coding sequences are

XX useful for stimulating an immune response in a patient, or for treating

XX prostate cancer in a patient and for determining, detecting or diagnosing

XX the presence of a cancer in a patient. The present sequence was used to

XX illustrate the invention

XX Sequence 318 AA:

Query Match 99.8%; Score 1619; DB 6; Length 318;
 Best Local Similarity 99.7%; Pred. No. 2.2e-169;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFLCSYLIVAGNLTIIYIVRTESLHE 60
 DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFLCSYLIVAGNLTIIYIVRTESLHE 60
 QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAIHSLSGMESTVLLA 120
 DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAIHSLSGMESTVLLA 120
 QY 121 MAFDRVVAICHPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIRKQLPFCRSNIIISHS 180
 DB 121 MAFDRVVAICHPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIRKQLPFCRSNIIISHS 180
 QY 181 YCLHODVMKLAACDDIRVVNVYGLIIVISAIGLDSLISFSYLLIKTVLGLTRBAQAKAF 240
 DB 181 YCLHODVMKLAACDDIRVVNVYGLIIVISAIGLDSLISFSYLLIKTVLGLTRBAQAKAF 240
 QY 241 GTCVSHCAVFIIVPPIGISMVHRFSKRDSPLPVLIANIYLLVPPVLPVIYGVYTKK 300
 DB 241 GTCVSHCAVFIIVPPIGISMVHRFSKRDSPLPVLIANIYLLVPPVLPVIYGVYTKK 300
 QY 301 IRORIILRFVATTHASEP 318
 DB 301 IRORIILRFVATTHASEP 318

RESULT 19

ABP81974 ID ABP81974 standard; protein; 318 AA.

AC ABP81974;
XX
XX 04-MAR-2003 (first entry)
DE Human G protein-coupled receptor L853440 protein SEQ ID NO:434.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM G protein-coupled receptor modulator; antibody; immune-related disease;
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM immunological-related cell proliferative disease; autoimmune disease;
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KM ulcer.
XX
XX Homo sapiens.
XX
XX WO200261087-A2.
XX
XX 08-AUG-2002.
XX
XX 19-DEC-2001; 2001WO-US050107.
XX
XX 19-DEC-2000; 2000US-0257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX Burner GC, Roush CL, Brown JP;
XX
XX WPI; 2003-046718/04.
XX
XX N-PSDB; ABZ42822.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (1) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptide and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention
XX
XX Sequence 318 AA;

Query Match 99.8%; Score 1619; DB 6; Length 318;
Best Local Similarity 99.7%; Pred. No. 2,2e-169;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYDPNGNESSATYFIILIGHGLEBAQFWLAFPLCSLYLNAVGNLTIIYVTRHSLHS 60
DB 1 MMYDPNGNESSATYFIILIGHGLEBAQFWLAFPLCSLYLNAVGNLTIIYVTRHSLHS 60
QY 61 PMYFLCMLSGIDILLISTSSMPKMLAFWNSSTTIQDACLQIFAIHSLSGHSTYLLA 120
DB 61 PMYFLCMLSGIDILLISTSSMPKMLAFWNSSTTIQDACLQIFAIHSLSGHSTYLLA 120
QY 121 MAPRYYAICHPRLHATVLTLPVYTKIGVAAVVGALMLPLPVFIQLPFCRSNLSHS 180
DB 121 MAPRYYAICHPRLHATVLTLPVYTKIGVAAVVGALMLPLPVFIQLPFCRSNLSHS 180
QY 181 YCLHQDVMKLAACDRIRVNYYGLVIIISAIQLDLSLISFSYLLILKTVLGLTRBAQKAP 240
DB 181 YCLHQDVMKLAACDRIRVNYYGLVIIISAIQLDLSLISFSYLLILKTVLGLTRBAQKAP 240
QY 241 GTCVSHVCAVFIYPVPITGSMVHRSKRSDSPVPLANIYLLVPVLAIPYGVYTKE 300
DB 241 GTCVSHVCAVFIYPVPITGSMVHRSKRSDSPVPLANIYLLVPVLAIPYGVYTKE 300
QY 301 IRORIILRFVATHASEP 318
DB 301 IRORIILRFVATHASEP 318

RESULT 20
ADB14370
ID ADB14370 standard; protein; 318 AA.
XX
XX ADB14370;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human prostate specific protein P835P.
XX
XX Human; prostate specific cDNA; cytosolic; immunostimulant; gene therapy;
XX cell therapy; vaccine; T-cell epitope;
XX class I major histocompatibility complex allele; MHC; prostate cancer;
XX tumour; antigen presenting cell.
XX
XX Homo sapiens.
XX
XX US2003185830-A1.
XX
XX 02-OCT-2003.
XX
XX 12-NOV-2002; 2002US-00294025.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00232149.
XX 15-JAN-1999; 99US-00288946.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX 14-JUN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.

PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852811.
PR 23-JUN-2001; 2001US-0085814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX (CORI-) CORIXA CORP.
PA
PI Xu J, Stolk JA, Kalos MD;
XX MPI; 2003-756193/71.
XX N-PSDB; ADB14366, ADB14368, ADB14369.
PT
PT New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
XX cancer.
XX
XX Example 15; Page; 101pp; English.
XX
XX The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC peptides comprise a fragment ADB13563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADB13558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating a cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a prostate specific
CC protein of the invention. Note: Except where otherwise indicated, the
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docid=20030185830.
XX
XX Sequence 318 AA;

Query Match 99.8%; Score 1619; DB 7; Length 318;
Best Local Similarity 99.7%; Pred. No. 2,2e-169;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIILIGPGLBBAQFWLAFPLCSLYLAVLGNLTIIYIVRTESLAE 60
DB 1 MMVDPNNGESSATYFIILIGPGLBBAQFWLAFPLCSLYLAVLGNLTIIYIVRTESLAE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFMFNSTTIOPDACLQJFAIHSLSGMSSTVLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFMFNSTTIOPDACLQJFAIHSLSGMSSTVLA 120
QY 121 MAFDRYVAICHPLRHATVLTLPVTKIGVAAVRGAALMAPLPVFIKQLPFCRSNIISSH 180
DB 121 MAFDRYVAICHPLRHATVLTLPVTKIGVAAVRGAALMAPLPVFIKQLPFCRSNIISSH 180

QY 181 YCLHODVMKLAACDIRNVVYGLIITISATGLSLISPSYLLILKTVLGLTREBAQAKAF 240
DB 181 YCLHODVMKLAACDIRNVVYGLIITISATGLSLISPSYLLILKTVLGLTREBAQAKAF 240
QY 241 GTCVSHVCAVFIYVFPFISLWHRFSKRDSPLVYLANIYLLVPEVLPNIYGVGVTKE 300
DB 241 GTCVSHVCAVFIYVFPFISLWHRFSKRDSPLVYLANIYLLVPEVLPNIYGVGVTKE 300
QY 301 IRORIILRFVHATPASEP 318
DB 301 IRORIILRFVHATPASEP 318

Search completed: March 9, 2006, 08:25:20
Job time : 192 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 9, 2006, 08:40:39 ; Search time 164 Seconds
(Without alignments)
810.181 Million cell updates/sec

Title: US-10-001-469a-2866
Perfect score: 1622
Sequence: 1 MMWDPMGNSSATYFILGL.....KEIRORILRLFHVATASAP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodaca/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodaca/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodaca/1/pubppaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodaca/1/pubppaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodaca/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1622	100.0	318	4	US-10-001-469-2880
2	1622	100.0	318	4	US-10-147-368-19
3	1622	100.0	318	4	US-10-147-368-28
4	1619	99.8	318	3	US-09-759-143-920
5	1619	99.8	318	3	US-09-780-669-920
6	1619	99.8	318	3	US-09-822-827-920
7	1619	99.8	318	3	US-09-886-055-91
8	1619	99.8	318	3	US-09-895-793-920
9	1619	99.8	318	3	US-09-895-814-920
10	1619	99.8	318	3	US-09-966-459A-2
11	1619	99.8	318	3	US-09-804-291-91
12	1619	99.8	318	4	US-10-012-896-920
13	1619	99.8	318	4	US-10-225-567A-434
14	1619	99.8	318	4	US-10-017-161-868
15	1619	99.8	318	4	US-10-144-678A-920
16	1619	99.8	318	4	US-10-294-025-920
17	1619	99.8	318	4	US-10-044-643-26
18	1619	99.8	318	4	US-10-147-368-32
19	1619	99.8	318	4	US-10-343-650A-158
20	1619	99.8	318	4	US-10-692-605-10
21	1619	99.8	318	4	US-10-323-412-2
22	1619	99.8	318	5	US-10-819-316-91
23	1617	99.7	317	4	US-10-205-823-443
24	1617	99.7	317	5	US-10-643-795A-125
25	1617	99.7	317	5	US-10-017-066-2
26	1617	99.7	317	5	US-10-948-518-125
27	1617	99.7	317	6	US-11-051-454-443

28	1614	99.5	317	4	US-10-295-027-873	Sequence 873, App
29	1614	99.5	317	4	US-10-292-798-746	Sequence 746, App
30	1612	99.4	318	4	US-10-044-643-28	Sequence 28, App
31	1612	99.4	318	4	US-10-044-643-30	Sequence 30, App
32	1610	99.3	316	4	US-10-147-368-33	Sequence 33, App
33	1542	95.1	303	4	US-10-001-469-2887	Sequence 2887, App
34	1534	94.6	302	4	US-10-001-469-2882	Sequence 2882, App
35	1515	93.4	298	4	US-10-001-469-2883	Sequence 2883, App
36	1515	93.4	298	4	US-10-001-469-2885	Sequence 2885, App
37	1515	93.4	298	4	US-10-147-368-35	Sequence 35, App
38	1515	93.4	298	4	US-10-147-368-37	Sequence 37, App
39	1512	93.2	316	4	US-10-147-368-34	Sequence 34, App
40	1512	93.2	317	5	US-10-774-355A-1329	Sequence 1329, App
41	1262	77.8	249	4	US-10-114-669-8894	Sequence 8894, App
42	985	60.7	320	4	US-10-005-041A-42	Sequence 42, App
43	985	60.7	320	5	US-10-774-355A-1347	Sequence 1347, App
44	979	60.4	318	4	US-10-024-399-18	Sequence 18, App
45	979	60.4	320	3	US-09-759-143-527	Sequence 527, App
46	979	60.4	320	3	US-09-730-018-7	Sequence 7, App
47	979	60.4	320	3	US-09-780-669-527	Sequence 527, App
48	979	60.4	320	3	US-09-822-827-527	Sequence 527, App
49	979	60.4	320	3	US-09-886-055-83	Sequence 83, App
50	979	60.4	320	3	US-09-968-033C-4	Sequence 4, App
51	979	60.4	320	3	US-09-895-793-527	Sequence 527, App
52	979	60.4	320	3	US-09-895-814-527	Sequence 527, App
53	979	60.4	320	3	US-09-804-291-83	Sequence 83, App
54	979	60.4	320	3	US-09-881-566A-55	Sequence 55, App
55	979	60.4	320	4	US-10-012-896-527	Sequence 527, App
56	979	60.4	320	4	US-10-081-775-4	Sequence 4, App
57	979	60.4	320	4	US-10-010-940-527	Sequence 527, App
58	979	60.4	320	4	US-10-205-823-337	Sequence 337, App
59	979	60.4	320	4	US-10-225-567A-662	Sequence 662, App
60	979	60.4	320	4	US-10-144-678A-527	Sequence 527, App
61	979	60.4	320	4	US-10-294-025-527	Sequence 527, App
62	979	60.4	320	4	US-10-431-842-7	Sequence 7, App
63	979	60.4	320	4	US-10-044-643-65	Sequence 65, App
64	979	60.4	320	4	US-10-025-806-34	Sequence 34, App
65	979	60.4	320	4	US-10-387-629-200	Sequence 200, App
66	979	60.4	320	4	US-10-005-041A-41	Sequence 41, App
67	979	60.4	320	4	US-10-343-650A-152	Sequence 152, App
68	979	60.4	320	5	US-10-968-294-4	Sequence 4, App
69	979	60.4	320	5	US-10-936-626-109	Sequence 109, App
70	979	60.4	320	5	US-10-938-061-109	Sequence 109, App
71	979	60.4	320	5	US-10-847-918-26	Sequence 26, App
72	979	60.4	320	5	US-10-819-316-83	Sequence 83, App
73	979	60.4	320	6	US-11-051-454-337	Sequence 337, App
74	979	60.4	368	4	US-10-106-698-6306	Sequence 6306, App
75	977.5	60.3	299	4	US-10-001-469-2886	Sequence 2886, App
76	977.5	60.3	299	4	US-10-147-368-38	Sequence 38, App
77	977	60.2	320	3	US-09-866-459A-12	Sequence 12, App
78	977	60.2	320	3	US-09-881-566A-53	Sequence 53, App
79	977	60.2	320	4	US-10-081-775-3	Sequence 3, App
80	977	60.2	320	4	US-10-044-643-64	Sequence 64, App
81	977	60.2	320	4	US-10-005-041A-44	Sequence 44, App
82	977	60.2	320	4	US-10-072-012-481	Sequence 481, App
83	977	60.2	320	4	US-10-323-412-12	Sequence 12, App
84	977	60.2	320	5	US-10-017-066-3	Sequence 3, App
85	975.5	60.1	299	4	US-10-001-469-2884	Sequence 2884, App
86	975.5	60.1	299	4	US-10-147-368-36	Sequence 36, App
87	967.5	59.6	322	5	US-10-774-355A-12409	Sequence 2409, App
88	965.5	59.5	320	5	US-09-968-033C-2	Sequence 2, App
89	965.5	59.5	320	5	US-10-968-294-2	Sequence 2, App
90	964.5	59.5	320	4	US-10-079-719-2	Sequence 2, App
91	964.5	59.5	320	4	US-10-097-340-123	Sequence 123, App
92	964.5	59.5	320	4	US-10-387-629-38	Sequence 38, App
93	964.5	59.5	320	5	US-10-017-066-4	Sequence 4, App
94	964.5	59.5	320	6	US-11-050-926-123	Sequence 123, App
95	937.5	57.8	316	4	US-10-023-601-42	Sequence 42, App
96	937.5	57.8	324	4	US-09-886-055-81	Sequence 81, App
97	937.5	57.8	324	4	US-09-804-291-81	Sequence 81, App
98	937.5	57.8	324	4	US-10-023-601-14	Sequence 14, App
99	937.5	57.8	324	4	US-10-387-629-204	Sequence 204, App
100	937.5	57.8	324	4	US-10-292-798-832	Sequence 832, App

ALIGNMENTS

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RESULT 1
US-10-001-469-2880
; Sequence 2880, Application US/10001469
; Publication No. US20030091562A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: HUBERT, RENE
; APPLICANT: PARIS, MARY
; APPLICANT: CHALLITA-ELD, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 101P3A11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.20
; CURRENT APPLICATION NUMBER: US/10/001,469
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/680,728
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2888
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2880
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 101P3A11 encoded amino
; US-10-001-469-2880

Query Match      100.0%; Score 1622; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.7e-151;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFIILIGLPGLEAOFWLAFLPCLSYLIVAGNLITIIYIVRTEHSLHE 60
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DB 1 MMVDPNGNESSATYFIILIGLPGLEAOFWLAFLPCLSYLIVAGNLITIIYIVRTEHSLHE 60
QY 61 PMYIFLCMTSGIDILISTSSMPKMLAIFWNSTTIOFDACLLQIPAHISLSGMESTVLLA 120
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DB 61 PMYIFLCMTSGIDILISTSSMPKMLAIFWNSTTIOFDACLLQIPAHISLSGMESTVLLA 120
QY 121 MAPRYYAICHPRHATVLTLPRTKIGVAAYVRGAAALMAPLVFPIKQLPFCRSNIIISHS 180
   |||||||
DB 121 MAPRYYAICHPRHATVLTLPRTKIGVAAYVRGAAALMAPLVFPIKQLPFCRSNIIISHS 180
QY 181 YCLHQDVWKLACDDIRVNVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
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DB 181 YCLHQDVWKLACDDIRVNVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHCAVFIYVPPFISGMVHRFSKRSDPLPVLIANTYLLVPPVLPNIYGVGTKE 300
   |||||||
DB 241 GTCVSHCAVFIYVPPFISGMVHRFSKRSDPLPVLIANTYLLVPPVLPNIYGVGTKE 300
QY 301 IRORIILRFVHATASBP 318
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DB 301 IRORIILRFVHATASBP 318

RESULT 2
US-10-147-368-19
; Sequence 19, Application US/10147368
; Publication No. US20030213004A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Paris
; APPLICANT: Arthur B. Raitano
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Douglas Saffran
; APPLICANT: Wangmao Ge
; APPLICANT: Pia M. Challita-ELD
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS
; TITLE OF INVENTION: ENTITLED 101P3A11 or PHOR-1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.21
; CURRENT APPLICATION NUMBER: US/10/147,368
; PRIOR APPLICATION NUMBER: US 10/017,066
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 10/001,469
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 09/680,728
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/157,902
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-147-368-19

Query Match      100.0%; Score 1622; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.7e-151;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFIILIGLPGLEAOFWLAFLPCLSYLIVAGNLITIIYIVRTEHSLHE 60
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DB 1 MMVDPNGNESSATYFIILIGLPGLEAOFWLAFLPCLSYLIVAGNLITIIYIVRTEHSLHE 60
QY 61 PMYIFLCMTSGIDILISTSSMPKMLAIFWNSTTIOFDACLLQIPAHISLSGMESTVLLA 120
   |||||||
DB 61 PMYIFLCMTSGIDILISTSSMPKMLAIFWNSTTIOFDACLLQIPAHISLSGMESTVLLA 120
QY 121 MAPRYYAICHPRHATVLTLPRTKIGVAAYVRGAAALMAPLVFPIKQLPFCRSNIIISHS 180
   |||||||
DB 121 MAPRYYAICHPRHATVLTLPRTKIGVAAYVRGAAALMAPLVFPIKQLPFCRSNIIISHS 180
QY 181 YCLHQDVWKLACDDIRVNVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
   |||||||
DB 181 YCLHQDVWKLACDDIRVNVVYGLIIVISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHCAVFIYVPPFISGMVHRFSKRSDPLPVLIANTYLLVPPVLPNIYGVGTKE 300
   |||||||
DB 241 GTCVSHCAVFIYVPPFISGMVHRFSKRSDPLPVLIANTYLLVPPVLPNIYGVGTKE 300
QY 301 IRORIILRFVHATASBP 318
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DB 301 IRORIILRFVHATASBP 318

RESULT 3
US-10-147-368-28
; Sequence 28, Application US/10147368
; Publication No. US20030213004A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Paris
; APPLICANT: Arthur B. Raitano
; APPLICANT: Robert Kendall Morrison
; APPLICANT: Douglas Saffran
; APPLICANT: Wangmao Ge
```

```
APPLICANT: Pia M. Chailita-Bid
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS
TITLE OF INVENTION: ENTITLED 101P3A11 OR PHOR-1 USEFUL IN TREATMENT AND
FILE REFERENCE: DETECTION OF CANCER
CURRENT APPLICATION NUMBER: US/10/147,368
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US 10/017,066
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 10/001,469
PRIOR FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US 60/291,118
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 09/680,728
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: US 60/157,902
PRIOR FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 318
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-147-368-28

Query Match      100.0%; Score 1622; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.7e-151;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFLLIGLPGLEAQPMLAFPLCSYLAVGNLTIIYVTEHSLH 60
DB 1 MMVDPNGNESSATYFLLIGLPGLEAQPMLAFPLCSYLAVGNLTIIYVTEHSLH 60
QY 61 PMYIFCLMSGIDILISTSSMPKMLAIFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFCLMSGIDILISTSSMPKMLAIFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
QY 121 MAFDRYVAICHPRHATVLTLPRTYKIGVAAVVRGALMLAPVPFIKOLPFCRSNIISHS 180
DB 121 MAFDRYVAICHPRHATVLTLPRTYKIGVAAVVRGALMLAPVPFIKOLPFCRSNIISHS 180
QY 181 YCHQDVYKACDIDIRNVVYGLIIVISAIGLDSLISFSYLLIKTVLGLTEBAQAKAF 240
DB 181 YCHQDVYKACDIDIRNVVYGLIIVISAIGLDSLISFSYLLIKTVLGLTEBAQAKAF 240
QY 241 GTCVSHVCAVFIFYVPFISGSMVHRFSKRDSPLPVILANIYLLVPVLPNIYGVYTKX 300
DB 241 GTCVSHVCAVFIFYVPFISGSMVHRFSKRDSPLPVILANIYLLVPVLPNIYGVYTKX 300
QY 301 IRRRIILRFVATTHASEP 318
DB 301 IRRRIILRFVATTHASEP 318

RESULT 4
US-09-759-143-920
Sequence 920, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kaloos, Michael D.
APPLICANT: Rafter, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
```

✓
920 =
pg 358

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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-759-143-920

Query Match      99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFLLIGLPGLEAQPMLAFPLCSYLAVGNLTIIYVTEHSLH 60
DB 1 MMVDPNGNESSATYFLLIGLPGLEAQPMLAFPLCSYLAVGNLTIIYVTEHSLH 60
QY 61 PMYIFCLMSGIDILISTSSMPKMLAIFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
DB 61 PMYIFCLMSGIDILISTSSMPKMLAIFWNSSTTIQPDACILQIFAIHSLSGMESTVLLA 120
QY 121 MAFDRYVAICHPRHATVLTLPRTYKIGVAAVVRGALMLAPVPFIKOLPFCRSNIISHS 180
DB 121 MAFDRYVAICHPRHATVLTLPRTYKIGVAAVVRGALMLAPVPFIKOLPFCRSNIISHS 180
QY 181 YCHQDVYKACDIDIRNVVYGLIIVISAIGLDSLISFSYLLIKTVLGLTEBAQAKAF 240
DB 181 YCHQDVYKACDIDIRNVVYGLIIVISAIGLDSLISFSYLLIKTVLGLTEBAQAKAF 240
QY 241 GTCVSHVCAVFIFYVPFISGSMVHRFSKRDSPLPVILANIYLLVPVLPNIYGVYTKX 300
DB 241 GTCVSHVCAVFIFYVPFISGSMVHRFSKRDSPLPVILANIYLLVPVLPNIYGVYTKX 300
QY 301 IRRRIILRFVATTHASEP 318
DB 301 IRRRIILRFVATTHASEP 318

RESULT 5
US-09-780-669-920
Sequence 920, Application US/09780669
Patent No. US2002005197A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kaloos, Michael D.
APPLICANT: Rafter, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurral, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
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6800746

;; CURRENT APPLICATION NUMBER: US/09/780,669
;; CURRENT FILING DATE: 2001-02-09
;; NUMBER OF SEQ ID NOS: 943
;; SOFTWARE: PaacSeq for Windows Version 3.0
;; SEQ ID NO 920
;; LENGTH: 318
;; TYPE: PR1
;; ORGANISM: Homo sapiens
US-09-780-669-920

Query Match 99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3,4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIYIVRTEHSLHE 60
DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIYIVRTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQPDACILQJFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQPDACILQJFAIHSLSGMESTVLLA 120
QY 121 MAFDRYVAICHPLRHAATVLTLPRTYTKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAFDRYVAICHPLRHAATVLTLPRTYTKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
QY 181 YCHLQDVMKACDDIRNVVYGLVIISAIGLSLISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCHLQDVMKACDDIRNVVYGLVIISAIGLSLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLPNIYVGVATKE 300
DB 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLPNIYVGVATKE 300
QY 301 IRQRILRLFHVATHASEP 318
DB 301 IRQRILRLFHVATHASEP 318

RESULT 6
US-09-822-827-920
;; Sequence 920, Application US/09822827
;; Patent No. US20020081680A1
;; GENERAL INFORMATION:
;; APPLICANT: Xu, Jiansheng
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.534C1
;; CURRENT APPLICATION NUMBER: US/09/822,827
;; CURRENT FILING DATE: 2001-03-28
;; NUMBER OF SEQ ID NOS: 982
;; SOFTWARE: PaacSeq for Windows Version 3.0
;; SEQ ID NO 920
;; LENGTH: 318
;; TYPE: PR1
;; ORGANISM: Homo sapiens
US-09-822-827-920

Query Match 99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3,4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIYIVRTEHSLHE 60
DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIYIVRTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQPDACILQJFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQPDACILQJFAIHSLSGMESTVLLA 120
QY 121 MAFDRYVAICHPLRHAATVLTLPRTYTKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAFDRYVAICHPLRHAATVLTLPRTYTKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180

QY 181 YCHLQDVMKACDDIRNVVYGLVIISAIGLSLISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCHLQDVMKACDDIRNVVYGLVIISAIGLSLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLPNIYVGVATKE 300
DB 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLPNIYVGVATKE 300
QY 301 IRQRILRLFHVATHASEP 318
DB 301 IRQRILRLFHVATHASEP 318

RESULT 7
US-09-886-055-91
;; Sequence 91, Application US/09886055
;; Patent No. US20020132273A1
;; GENERAL INFORMATION:
;; APPLICANT: STRYER, LUBERT
;; APPLICANT: ZOZULYA, SERGEY
;; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
;; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
;; FILE REFERENCE: 078003-0277150
;; CURRENT APPLICATION NUMBER: US/09/886,055
;; CURRENT FILING DATE: 2001-06-22
;; PRIOR APPLICATION NUMBER: 60/213,812
;; PRIOR FILING DATE: 2000-06-22
;; NUMBER OF SEQ ID NOS: 522
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 91
;; LENGTH: 318
;; TYPE: PR1
;; ORGANISM: Homo sapiens
US-09-886-055-91

Query Match 99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3,4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIYIVRTEHSLHE 60
DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIYIVRTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQPDACILQJFAIHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWFNSTTIQPDACILQJFAIHSLSGMESTVLLA 120
QY 121 MAFDRYVAICHPLRHAATVLTLPRTYTKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAFDRYVAICHPLRHAATVLTLPRTYTKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
QY 181 YCHLQDVMKACDDIRNVVYGLVIISAIGLSLISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCHLQDVMKACDDIRNVVYGLVIISAIGLSLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLPNIYVGVATKE 300
DB 241 GTCVSHVCAVFIFFVPPFGLSMVHRFSKRSDPLPVILANIYLLVPPVLPNIYVGVATKE 300
QY 301 IRQRILRLFHVATHASEP 318
DB 301 IRQRILRLFHVATHASEP 318

RESULT 8
US-09-895-793-920
;; Sequence 920, Application US/09895793
;; Publication No. US20020192763A1
;; GENERAL INFORMATION:
;; APPLICANT: Xu, Jiansheng
;; APPLICANT: Dillon, Devin C.
;; APPLICANT: Mitcham, Jennifer L.

```

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugtu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-793-920
```

```

Query Match          99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3,4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAPLCSLYLAVGNLTIIYIVTRESLHE 60
DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAPLCSLYLAVGNLTIIYIVTRESLHE 60
QY 61 PMTIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAHISLSGNESTVLLA 120
DB 61 PMTIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAHISLSGNESTVLLA 120
QY 121 MAFDRYVAICHPRHATVLTLPRTYKIGVAAVVRGALMAPLVFIKQLPFCRSNIIISHS 180
DB 121 MAFDRYVAICHPRHATVLTLPRTYKIGVAAVVRGALMAPLVFIKQLPFCRSNIIISHS 180
QY 181 YCHQDVWKACDIDIRNVVYGLIIVISAGLDSLISFSYLLILKTVLGLTREBAQKAF 240
DB 181 YCHQDVWKACDIDIRNVVYGLIIVISAGLDSLISFSYLLILKTVLGLTREBAQKAF 240
QY 241 GTCVSHVCAVFIFYVPFISGWSVHRFSKRRDSPLVILANIYLLVPPVLPVIYGVYTKE 300
DB 241 GTCVSHVCAVFIFYVPFISGWSVHRFSKRRDSPLVILANIYLLVPPVLPVIYGVYTKE 300
QY 301 IRRRIILRFHVATHASEP 318
DB 301 IRRRIILRFHVATHASEP 318
```

```

RESULT 9
US-09-895-814-920
; Sequence 920, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaangehun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugtu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
```

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; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-814-920
```

```

Query Match          99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3,4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAPLCSLYLAVGNLTIIYIVTRESLHE 60
DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAPLCSLYLAVGNLTIIYIVTRESLHE 60
QY 61 PMTIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAHISLSGNESTVLLA 120
DB 61 PMTIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACLQIFAHISLSGNESTVLLA 120
QY 121 MAFDRYVAICHPRHATVLTLPRTYKIGVAAVVRGALMAPLVFIKQLPFCRSNIIISHS 180
DB 121 MAFDRYVAICHPRHATVLTLPRTYKIGVAAVVRGALMAPLVFIKQLPFCRSNIIISHS 180
QY 181 YCHQDVWKACDIDIRNVVYGLIIVISAGLDSLISFSYLLILKTVLGLTREBAQKAF 240
DB 181 YCHQDVWKACDIDIRNVVYGLIIVISAGLDSLISFSYLLILKTVLGLTREBAQKAF 240
QY 241 GTCVSHVCAVFIFYVPFISGWSVHRFSKRRDSPLVILANIYLLVPPVLPVIYGVYTKE 300
DB 241 GTCVSHVCAVFIFYVPFISGWSVHRFSKRRDSPLVILANIYLLVPPVLPVIYGVYTKE 300
QY 301 IRRRIILRFHVATHASEP 318
DB 301 IRRRIILRFHVATHASEP 318
```

```

RESULT 10
US-09-966-459A-2
; Sequence 2, Application US/09966459A
; Publication No. US2003002237A1
; GENERAL INFORMATION:
; APPLICANT: FESDER, J.N.
; APPLICANT: MINTER, G.
; APPLICANT: RAMANATHAN, C.S.
; APPLICANT: HAWKEN, D.R.
; APPLICANT: CACACE, A.
; APPLICANT: BARBER, L.
; APPLICANT: KORNAKNER, M.G.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HEPREMY4,
; FILE REFERENCE: D0039NP
; CURRENT APPLICATION NUMBER: US/09/966,459A
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```

; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,833
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,776
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/305,351
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/313,202
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-459a.2

Query Match          99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3,4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIYIVRTESLHE 60
   |||
DB 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIYIVRTESLHE 60

QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWNSSTTIQFDACLLQIFAHSLSGMESTVLLA 120
   |||
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWNSSTTIQFDACLLQIFAHSLSGMESTVLLA 120

QY 121 MAFDRYVAICHPLRHATVTLPRVTKIGVAAVRGAAALMAPLPVFIKQLPFCRSNIIISHS 180
   |||
DB 121 MAFDRYVAICHPLRHATVTLPRVTKIGVAAVRGAAALMAPLPVFIKQLPFCRSNIIISHS 180

QY 181 YCLHODVMKLAACDRIRVNVVYGLVIISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
   |||
DB 181 YCLHODVMKLAACDRIRVNVVYGLVIISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240

QY 241 GTCVSHCAVFIFFVPTIGLSMVRFSKRSDPLPVLANIYLLVPPVLANPIYGVGTKE 300
   |||
DB 241 GTCVSHCAVFIFFVPTIGLSMVRFSKRSDPLPVLANIYLLVPPVLANPIYGVGTKE 300

QY 301 IRRRIILRFHVATHASEP 318
   |||
DB 301 IRRRIILRFHVATHASEP 318

RESULT 11
US-09-804-291-91
; Sequence 91, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZILA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
```

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; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-291-91

Query Match          99.8%; Score 1619; DB 3; Length 318;
Best Local Similarity 99.7%; Pred. No. 3,4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIYIVRTESLHE 60
   |||
DB 1 MMVDPNNGESSATYFIILIGLPGLEBAQFWLAFPLCSLYLNAVGNLTIYIVRTESLHE 60

QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWNSSTTIQFDACLLQIFAHSLSGMESTVLLA 120
   |||
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIFWNSSTTIQFDACLLQIFAHSLSGMESTVLLA 120

QY 121 MAFDRYVAICHPLRHATVTLPRVTKIGVAAVRGAAALMAPLPVFIKQLPFCRSNIIISHS 180
   |||
DB 121 MAFDRYVAICHPLRHATVTLPRVTKIGVAAVRGAAALMAPLPVFIKQLPFCRSNIIISHS 180

QY 181 YCLHODVMKLAACDRIRVNVVYGLVIISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240
   |||
DB 181 YCLHODVMKLAACDRIRVNVVYGLVIISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240

QY 241 GTCVSHCAVFIFFVPTIGLSMVRFSKRSDPLPVLANIYLLVPPVLANPIYGVGTKE 300
   |||
DB 241 GTCVSHCAVFIFFVPTIGLSMVRFSKRSDPLPVLANIYLLVPPVLANPIYGVGTKE 300

QY 301 IRRRIILRFHVATHASEP 318
   |||
DB 301 IRRRIILRFHVATHASEP 318

RESULT 12
US-10-012-896-920
; Sequence 920, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Baebols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
```

SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 920
 LENGTH: 318
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-012-896-920

Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. No. 3.4e-151;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFILIGLPGLEBAQFWLAFLCSLYLAVGNLTITIVYVTEHSLH 60
 DB 1 MMVDPNNGESSATYFILIGLPGLEBAQFWLAFLCSLYLAVGNLTITIVYVTEHSLH 60
 QY 61 PMYFLCMLSGIDILISTSSMPKMLAIFWNSTTIQPDACLLQWFAHSLSGMESTVLLA 120
 DB 61 PMYFLCMLSGIDILISTSSMPKMLAIFWNSTTIQPDACLLQWFAHSLSGMESTVLLA 120
 QY 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
 DB 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
 QY 181 YCHLDQVWKLACDDIRVNVVYGLIVIIISAGLSLISFSYLLILKTVLGLTREAOAKAF 240
 DB 181 YCHLDQVWKLACDDIRVNVVYGLIVIIISAGLSLISFSYLLILKTVLGLTREAOAKAF 240
 QY 241 GTCVSHCAVFIYPVPFGLSMVHRSKRSDPLPVILANIYLLVPPVLPNIYVGVTKKE 300
 DB 241 GTCVSHCAVFIYPVPFGLSMVHRSKRSDPLPVILANIYLLVPPVLPNIYVGVTKKE 300
 QY 301 IRRRIILRFHVATASEP 318
 DB 301 IRRRIILRFHVATASEP 318

RESULT 13
 US-10-225-567A-434

; Sequence 434, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lifespan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 434
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-225-567A-434

Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. No. 3.4e-151;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFILIGLPGLEBAQFWLAFLCSLYLAVGNLTITIVYVTEHSLH 60
 DB 1 MMVDPNNGESSATYFILIGLPGLEBAQFWLAFLCSLYLAVGNLTITIVYVTEHSLH 60
 QY 61 PMYFLCMLSGIDILISTSSMPKMLAIFWNSTTIQPDACLLQWFAHSLSGMESTVLLA 120
 DB 61 PMYFLCMLSGIDILISTSSMPKMLAIFWNSTTIQPDACLLQWFAHSLSGMESTVLLA 120
 QY 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
 DB 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180

DB 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
 QY 181 YCHLDQVWKLACDDIRVNVVYGLIVIIISAGLSLISFSYLLILKTVLGLTREAOAKAF 240
 DB 181 YCHLDQVWKLACDDIRVNVVYGLIVIIISAGLSLISFSYLLILKTVLGLTREAOAKAF 240
 QY 241 GTCVSHCAVFIYPVPFGLSMVHRSKRSDPLPVILANIYLLVPPVLPNIYVGVTKKE 300
 DB 241 GTCVSHCAVFIYPVPFGLSMVHRSKRSDPLPVILANIYLLVPPVLPNIYVGVTKKE 300
 QY 301 IRRRIILRFHVATASEP 318
 DB 301 IRRRIILRFHVATASEP 318

RESULT 14
 US-10-017-161-868

; Sequence 868, Application US/10017161
 ; Publication No. US20030143668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUMA, MAKIKO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: ABEYATANI, HIROYUKI
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 084335/0152
 ; CURRENT APPLICATION NUMBER: US/10/017,161
 ; PRIOR FILING DATE: 2002-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001/246789
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ ID NOS: 2430
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 868
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-017-161-868

Query Match 99.8%; Score 1619; DB 4; Length 318;
 Best Local Similarity 99.7%; Pred. No. 3.4e-151;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNNGESSATYFILIGLPGLEBAQFWLAFLCSLYLAVGNLTITIVYVTEHSLH 60
 DB 1 MMVDPNNGESSATYFILIGLPGLEBAQFWLAFLCSLYLAVGNLTITIVYVTEHSLH 60
 QY 61 PMYFLCMLSGIDILISTSSMPKMLAIFWNSTTIQPDACLLQWFAHSLSGMESTVLLA 120
 DB 61 PMYFLCMLSGIDILISTSSMPKMLAIFWNSTTIQPDACLLQWFAHSLSGMESTVLLA 120
 QY 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
 DB 121 MAFPRYVAICHPLEHATVLTLPRTYKIGVAAVVRGAAALMAPLPVFIKQLPFCRSNIISHS 180
 QY 181 YCHLDQVWKLACDDIRVNVVYGLIVIIISAGLSLISFSYLLILKTVLGLTREAOAKAF 240
 DB 181 YCHLDQVWKLACDDIRVNVVYGLIVIIISAGLSLISFSYLLILKTVLGLTREAOAKAF 240
 QY 241 GTCVSHCAVFIYPVPFGLSMVHRSKRSDPLPVILANIYLLVPPVLPNIYVGVTKKE 300
 DB 241 GTCVSHCAVFIYPVPFGLSMVHRSKRSDPLPVILANIYLLVPPVLPNIYVGVTKKE 300
 QY 301 IRRRIILRFHVATASEP 318
 DB 301 IRRRIILRFHVATASEP 318

RESULT 15
 US-10-144-678A-920

; Sequence 920, Application US/10144678A
 ; Publication No. US20030157089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jlangchun

APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kaios, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinales y de Bascoles, Carlotca
APPLICANT: Foy, Teresa M.
APPLICANT: Matanabe, Yoshinhiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-678A-920

Query Match 99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMDPNGNESSATYFIILIGLPGLEBAQFWLAPFLCSLYLIANGLNTIYIVRTEHSLHE 60
DB 1 MMDPNGNESSATYFIILIGLPGLEBAQFWLAPFLCSLYLIANGLNTIYIVRTEHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWPNSTTIQPDACLOMPALHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWPNSTTIQPDACLOMPALHSLSGMESTVLLA 120
QY 121 MAPDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISSH 180
DB 121 MAPDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISSH 180
QY 181 YCHQDWKLAACDDIRVNVVGLIYISAIIGDSLISFSYLLIKTYLGLTREAOAKAF 240
DB 181 YCHQDWKLAACDDIRVNVVGLIYISAIIGDSLISFSYLLIKTYLGLTREAOAKAF 240
QY 241 GTCVSHCAVPIFYVPPIGLSMVHRFSKRSDPLVILANTYLLVPLNPIYGVKTKX 300
DB 241 GTCVSHCAVPIFYVPPIGLSMVHRFSKRSDPLVILANTYLLVPLNPIYGVKTKX 300
QY 301 IRQRILRLFHVATASEP 318
DB 301 IRQRILRLFHVATASEP 318

RESULT 16
US-10-294-025-920
Sequence 920, Application US/10294025
Publication No. US20030185830A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Kaios, Michael D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C29
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-294-025-920

Query Match 99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWPNSTTIQPDACLOMPALHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWPNSTTIQPDACLOMPALHSLSGMESTVLLA 120
QY 121 MAPDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISSH 180
DB 121 MAPDRYVAICHPLRHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISSH 180
QY 181 YCHQDWKLAACDDIRVNVVGLIYISAIIGDSLISFSYLLIKTYLGLTREAOAKAF 240
DB 181 YCHQDWKLAACDDIRVNVVGLIYISAIIGDSLISFSYLLIKTYLGLTREAOAKAF 240
QY 241 GTCVSHCAVPIFYVPPIGLSMVHRFSKRSDPLVILANTYLLVPLNPIYGVKTKX 300
DB 241 GTCVSHCAVPIFYVPPIGLSMVHRFSKRSDPLVILANTYLLVPLNPIYGVKTKX 300
QY 301 IRQRILRLFHVATASEP 318
DB 301 IRQRILRLFHVATASEP 318

RESULT 17
US-10-044-643-26
Sequence 26, Application US/10044643
Publication No. US20030195335A1
GENERAL INFORMATION:
APPLICANT: Majumder, Kumud
APPLICANT: Vermet, Corine
APPLICANT: Caeman, Stacie J
APPLICANT: Wolenc, Adam R
APPLICANT: Spaderna, Steven K
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mishra, Vishnu S
APPLICANT: Tchernev, Velizar T
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Baumgartner, Jason C
APPLICANT: Guev, Vladimir
TITLE OF INVENTION: No. US20030195335A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-748
CURRENT APPLICATION NUMBER: US/10/044,643
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 60/193,664
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/194,614
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,063
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,066
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,067
PRIOR FILING DATE: 2000-04-06


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; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 60/221,284
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/221,325
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/224,588
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/239,613
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 60/262,508
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,604
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,433
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/265,161
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-643-26
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Query Match          99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MMVDPNENSSATYFLLIGLPGLEAOPMLAFPLCSYLLAVNGNTLTIYVREHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWENSTTIQPDACILQIFAIHSHSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWENSTTIQPDACILQIFAIHSHSGMESTVLLA 120
QY 121 MAFDRYVAICHPLRHATVTLPRVTXIGVAAVVRGAALMAPLVFIKQLPFCRSNIISHS 180
DB 121 MAFDRYVAICHPLRHATVTLPRVTXIGVAAVVRGAALMAPLVFIKQLPFCRSNIISHS 180
QY 181 YCHLQDVWKLAACDDIRNVVYGLIYIISALGDSLLISFSYLLILKTVLGLTREAOAKAF 240
DB 181 YCHLQDVWKLAACDDIRNVVYGLIYIISALGDSLLISFSYLLILKTVLGLTREAOAKAF 240
QY 241 GTCVSHVCAVFIFVVPPIGSMVHRFSKRDSPLPVILANIYLLVPPVLPYVGVYTKS 300
DB 241 GTCVSHVCAVFIFVVPPIGSMVHRFSKRDSPLPVILANIYLLVPPVLPYVGVYTKS 300
QY 301 IRORIILRLFHVATHASEP 318
DB 301 IRORIILRLFHVATHASEP 318
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RESULT 18
US-10-147-368-32
; Sequence 32, Application US/10147368
; Publication No. US20030213004A1
; GENERAL INFORMATION:
; APPLICANT: Agemys, Inc.
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Paris
; APPLICANT: Arthur B. Raitano
; APPLICANT: Robert Kendall Morrison
```

```
; APPLICANT: Douglas Saffran
; APPLICANT: Wangmao Ge
; APPLICANT: Pia M. Chailita-Eid
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS
; TITLE OF INVENTION: ENTITLED 101P3A11 OR PHOR-1 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20024.21
; CURRENT APPLICATION NUMBER: US/10/147,368
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 10/017,066
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 10/001,469
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 09/680,728
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/157,902
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: RabsSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-147-368-32
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Query Match          99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 301 IRORIILRLFHVATHASEP 318
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RESULT 19
US-10-343-650A-158
; Sequence 158, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HACA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
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; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-158

Query Match      99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFLPCSLYLIAVGNLTIIYIVRTEHSLHE 60

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QY 121 MAPDRYVAICHPLRHATVLTLPRTYTKIGVAAVVGAALMAPLPVFIRKQLPFCRSNIISHS 180
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DB 121 MAPDRYVAICHPLRHATVLTLPRTYTKIGVAAVVGAALMAPLPVFIRKQLPFCRSNIISHS 180

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   |||||
DB 181 YCLHODVMKLAACDRIRVNVVYGLIYIISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240

QY 241 GTCVSHVCAVPIFYVPPFISLMSVHRFSKRSDSPLPVILANIYLLVPPVLANPIYVGVTKE 300
   |||||
DB 241 GTCVSHVCAVPIFYVPPFISLMSVHRFSKRSDSPLPVILANIYLLVPPVLANPIYVGVTKE 300

QY 301 IRQRILRLFHVATHASEP 318
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DB 301 IRQRILRLFHVATHASEP 318
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RESULT 20
US-10-692-605-10
; Sequence 10, Application US/10692605
; Publication No. US20040091928A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S.
; APPLICANT: Merchant, Kaipana
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN
; FILE REFERENCE: 28341/6276.NX1
; CURRENT APPLICATION NUMBER: US/10/692,605
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US 09/698,419
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 09/481,794
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 09/454,399
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 09/429,517
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,555
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,676
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,695
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/428,114
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/428,020
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/427,859
; PRIOR FILING DATE: 1999-10-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-692-605-10

Query Match      99.8%; Score 1619; DB 4; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.4e-151;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MMVDPNNGESSATYFIIIGLPGLEBAQFWLAFLPCSLYLIAVGNLTIIYIVRTEHSLHE 60

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DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWFNSTTIQPDACILQWFAHSLSGMESTVLLA 120

QY 121 MAPDRYVAICHPLRHATVLTLPRTYTKIGVAAVVGAALMAPLPVFIRKQLPFCRSNIISHS 180
   |||||
DB 121 MAPDRYVAICHPLRHATVLTLPRTYTKIGVAAVVGAALMAPLPVFIRKQLPFCRSNIISHS 180

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   |||||
DB 181 YCLHODVMKLAACDRIRVNVVYGLIYIISAIGLDSLISFSYLLILKTVLGLTREAOAKAF 240

QY 241 GTCVSHVCAVPIFYVPPFISLMSVHRFSKRSDSPLPVILANIYLLVPPVLANPIYVGVTKE 300
   |||||
DB 241 GTCVSHVCAVPIFYVPPFISLMSVHRFSKRSDSPLPVILANIYLLVPPVLANPIYVGVTKE 300

QY 301 IRQRILRLFHVATHASEP 318
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DB 301 IRQRILRLFHVATHASEP 318
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Search completed: March 9, 2006, 08:43:56
Job time : 166 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 9, 2006, 08:41:19 ; Search time 22 Seconds
(without alignments)
402.341 Million cell updates/sec

Title: US-10-001-469a-2866

Perfect score: 1622

Sequence: 1 MWVDPMNGESSATYFILIGL.....KEIKRRIILRFVATASEP 318

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Searched: 161667 seqs, 2783485 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA New:*
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2: /cgn2_6/ptcdaca/1/pubppaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	868.5	53.5	312	6	US-10-055-877-339
4	827.5	51.0	315	7	US-11-190-188-8
5	812.5	50.1	314	6	US-10-511-538-70
6	799.5	49.3	342	6	US-10-055-877-335
7	771	47.5	311	7	US-11-190-188-10
8	758.5	46.8	321	6	US-10-055-877-338
9	742	45.7	356	7	US-11-150-188-9
10	737.5	45.5	312	7	US-11-124-367A-496
11	736.5	45.4	312	7	US-11-124-367A-514
12	726.5	44.8	303	6	US-10-055-877-123
13	718.5	44.3	327	6	US-10-055-877-337
14	648	40.0	321	6	US-10-511-538-225
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24	447.5	27.6	314	6	US-10-055-877-56
25	443.5	27.3	319	6	US-10-055-877-221

26	442.5	27.3	318	6	US-10-055-877-324	Sequence 324, App
27	442	27.3	311	6	US-10-511-538-176	Sequence 176, App
28	439.5	27.1	453	7	US-11-190-188-19	Sequence 19, App
29	435.5	26.8	318	6	US-10-055-877-323	Sequence 323, App
30	429.5	26.5	315	7	US-11-241-956-15	Sequence 15, App
31	429.5	26.5	491	6	US-10-511-538-48	Sequence 48, App
32	427.5	26.4	312	7	US-11-241-956-12	Sequence 12, App
33	426.5	26.3	315	7	US-11-241-956-11	Sequence 11, App
34	419.5	25.9	314	6	US-10-511-538-153	Sequence 153, App
35	418	25.8	309	7	US-11-241-956-13	Sequence 13, App
36	411.5	25.4	311	7	US-11-190-188-15	Sequence 15, App
37	409.5	25.2	313	7	US-11-095-093-2	Sequence 2, App
38	407	25.1	310	6	US-10-511-538-215	Sequence 215, App
39	406.5	25.0	319	7	US-11-190-188-14	Sequence 14, App
40	405.5	25.0	312	7	US-10-511-538-26	Sequence 26, App
41	405.5	25.0	312	7	US-11-124-368A-330	Sequence 330, App
42	400.5	24.7	307	6	US-10-055-877-62	Sequence 62, App
43	400.5	24.7	307	6	US-10-055-877-232	Sequence 232, App
44	400.5	24.7	309	7	US-11-190-188-13	Sequence 13, App
45	400.5	24.7	318	6	US-10-055-877-119	Sequence 119, App
46	400.5	24.7	318	6	US-10-055-877-322	Sequence 322, App
47	399.5	24.6	310	6	US-10-511-538-217	Sequence 217, App
48	396	24.4	308	6	US-10-055-877-235	Sequence 235, App
49	395	24.4	318	6	US-10-511-538-163	Sequence 163, App
50	395	24.4	318	7	US-11-190-188-21	Sequence 21, App
51	394.5	24.3	298	6	US-10-511-538-186	Sequence 186, App
52	393	24.2	316	7	US-11-190-188-18	Sequence 18, App
53	390	24.0	313	7	US-11-190-188-7	Sequence 7, App
54	388.5	24.0	316	7	US-11-190-188-17	Sequence 17, App
55	387	23.9	308	6	US-10-055-877-233	Sequence 233, App
56	387	23.8	313	6	US-10-055-877-234	Sequence 234, App
57	386.5	23.8	307	7	US-11-241-956-16	Sequence 16, App
58	386.5	23.8	312	6	US-10-511-538-97	Sequence 97, App
59	383.5	23.6	309	6	US-10-511-538-188	Sequence 188, App
60	376	23.2	313	6	US-10-511-538-64	Sequence 64, App
61	374	23.1	277	6	US-10-055-877-236	Sequence 236, App
62	370	22.8	314	7	US-11-190-188-16	Sequence 16, App
63	365.5	22.5	306	6	US-10-511-538-182	Sequence 182, App
64	353.5	21.8	323	6	US-10-511-538-168	Sequence 168, App
65	353.5	21.8	323	7	US-11-190-188-20	Sequence 20, App
66	351	21.6	308	6	US-10-511-538-219	Sequence 219, App
67	344.5	21.2	313	6	US-10-511-538-13	Sequence 13, App
68	332	20.5	268	6	US-10-511-538-7	Sequence 7, App
69	309	19.0	354	7	US-11-190-188-11	Sequence 11, App
70	308	19.0	309	7	US-11-241-956-14	Sequence 14, App
71	262	16.2	280	6	US-10-511-538-2	Sequence 2, App
72	248	15.3	240	6	US-10-511-538-41	Sequence 41, App
73	184.5	11.4	317	6	US-10-995-561-798	Sequence 78, App
74	184.5	11.4	318	7	US-11-127-877-38	Sequence 38, App
75	184.5	11.4	797	6	US-10-995-561-802	Sequence 802, App
76	183.5	11.3	173	6	US-10-511-538-190	Sequence 190, App
77	180	11.1	325	7	US-11-166-412-65	Sequence 65, App
78	174.5	10.8	350	6	US-10-995-561-547	Sequence 547, App
79	161	9.9	144	7	US-11-000-463-376	Sequence 376, App
80	160.5	9.9	360	6	US-10-959-310-36	Sequence 36, App
81	160.5	9.9	360	7	US-11-144-731-1	Sequence 36, App
82	159	9.8	347	7	US-11-174-816-42	Sequence 42, App
83	159	9.8	347	7	US-11-174-819-9	Sequence 9, App
84	158	9.7	359	6	US-10-330-773-930	Sequence 90, App
85	156	9.6	259	6	US-10-055-877-227	Sequence 225, App
86	156	9.6	259	6	US-10-055-877-237	Sequence 237, App
87	156	9.6	259	7	US-11-206-587-27	Sequence 27, App
88	156	9.6	259	7	US-11-206-587-29	Sequence 29, App
89	156	9.6	412	7	US-11-170-153-4	Sequence 4, App
90	156	9.6	412	7	US-11-170-166-4	Sequence 4, App
91	156	9.6	412	7	US-11-170-351-1	Sequence 1, App
92	156	9.6	415	7	US-11-170-153-2	Sequence 2, App
93	156	9.6	415	7	US-11-170-166-2	Sequence 2, App
94	156	9.6	415	7	US-11-170-351-2	Sequence 2, App
95	155	9.6	347	7	US-11-174-816-57	Sequence 57, App
96	155	9.6	347	7	US-11-174-819-76	Sequence 76, App
97	154	9.5	381	6	US-10-987-856-16	Sequence 16, App
98	153	9.4	360	6	US-10-851-677A-26	Sequence 26, App

99 152 9.4 360 6 US-10-330-773-933 Sequence 933, App
100 151 9.3 149 6 US-10-511-538-172 Sequence 172, App

ALIGNMENTS

RESULT 1

US-11-234-786-527

Sequence 527, Application US/11234786

Publication No. US20060024301A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, David C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Reed, Steven G.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darick

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skelky, Yasir A.

TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION

FILE OF INVENTION: POLYPEPTIDES THEROF

FILE REFERENCE: 210121.427C31

CURRENT APPLICATION NUMBER: US/11/234,786

CURRENT FILING DATE: 2005-09-23

PRIOR APPLICATION NUMBER: US 09/568,857

PRIOR FILING DATE: 2000-05-09

PRIOR APPLICATION NUMBER: US 09/536,857

PRIOR FILING DATE: 2000-05-27

PRIOR APPLICATION NUMBER: US 09/483,672

PRIOR FILING DATE: 2000-01-14

PRIOR APPLICATION NUMBER: US 09/439,313

PRIOR FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: US 09/352,616

PRIOR FILING DATE: 1999-07-13

PRIOR APPLICATION NUMBER: US 09/288,946

PRIOR FILING DATE: 1999-04-09

PRIOR APPLICATION NUMBER: US 09/232,149

PRIOR FILING DATE: 1999-01-15

PRIOR APPLICATION NUMBER: US 09/159,812

PRIOR FILING DATE: 1998-09-23

PRIOR APPLICATION NUMBER: US 09/115,453

PRIOR FILING DATE: 1998-07-14

PRIOR APPLICATION NUMBER: US 09/030,607

PRIOR FILING DATE: 1998-02-25

Remaining Prior Application data removed - See file Wrapper or PALM.

NUMBER OF SEQ ID NOS: 701

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 527

LENGTH: 320

TYPE: PRT

ORGANISM: Homo sapiens

US-11-234-786-527

Query Match

Best Local Similarity 59.5%, Score 979, DB 7, Length 320;

Matches 182, Conservative 55, Mismatches 67, Indels 2, Gaps 2;

Cy

Db

Cy

Db

Cy

Db

Cy

Db

Cy

Db

Cy

Sequence 933, App
Sequence 172, App

ALIGNMENTS

RESULT 2

US-10-055-877-336

Sequence 336, Application US/10055877

Publication No. US20050288241A1

GENERAL INFORMATION:

APPLICANT: Decristofaro, Marc

APPLICANT: Padigaru, Muralidhara

APPLICANT: Miller, Charles

APPLICANT: Tchernev, Velizar

APPLICANT: Zhong, Mei

APPLICANT: Anderson, David

APPLICANT: Ballinger, Robert

APPLICANT: Gerlach, Valerie

APPLICANT: Spytek, Kimberly

APPLICANT: Rattelli, Luca

APPLICANT: Kekuda, Ramesh

APPLICANT: Guo, Xiaojia

APPLICANT: Zethusen, Bryan

APPLICANT: Andrew, David

APPLICANT: Mezes, Peter

APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine

APPLICANT: Eileen, Andrew

APPLICANT: Wolenc, Adam

APPLICANT: Baumgartner, Jason

APPLICANT: Shimkets, Richard

APPLICANT: Gusev, Vladimir

APPLICANT: Vernet, Corinne

APPLICANT: Taupier Jr., Raymond

APPLICANT: Pena, Carol

APPLICANT: Shenoy, Suresh

APPLICANT: Li, Li

APPLICANT: Caeman, Stacie

APPLICANT: Boidog, Ference

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby

FILE REFERENCE: 21402-251

CURRENT APPLICATION NUMBER: US/10/055,877

CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: 60/262,892

PRIOR FILING DATE: 2001-01-19

PRIOR APPLICATION NUMBER: 60/263,598

PRIOR FILING DATE: 2001-01-23

PRIOR APPLICATION NUMBER: 60/263,799

PRIOR FILING DATE: 2001-01-24

PRIOR APPLICATION NUMBER: 60/264,117

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 60/264,139

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 60/264,478

PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/263,351

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/272,870

PRIOR FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 60/275,990

Query Match

Best Local Similarity 59.5%, Score 979, DB 7, Length 320;

Matches 182, Conservative 55, Mismatches 67, Indels 2, Gaps 2;

Cy

Db

Cy

Db

Cy

Db

Cy

Db

Cy

Db

Sequence 933, App
Sequence 172, App

ALIGNMENTS

RESULT 2

US-10-055-877-336

Sequence 336, Application US/10055877

Publication No. US20050288241A1

GENERAL INFORMATION:

APPLICANT: Decristofaro, Marc

APPLICANT: Padigaru, Muralidhara

APPLICANT: Miller, Charles

APPLICANT: Tchernev, Velizar

APPLICANT: Zhong, Mei

APPLICANT: Anderson, David

APPLICANT: Ballinger, Robert

APPLICANT: Gerlach, Valerie

APPLICANT: Spytek, Kimberly

APPLICANT: Rattelli, Luca

APPLICANT: Kekuda, Ramesh

APPLICANT: Guo, Xiaojia

APPLICANT: Zethusen, Bryan

APPLICANT: Andrew, David

APPLICANT: Mezes, Peter

APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine

APPLICANT: Eileen, Andrew

APPLICANT: Wolenc, Adam

APPLICANT: Baumgartner, Jason

APPLICANT: Shimkets, Richard

APPLICANT: Gusev, Vladimir

APPLICANT: Vernet, Corinne

APPLICANT: Taupier Jr., Raymond

APPLICANT: Pena, Carol

APPLICANT: Shenoy, Suresh

APPLICANT: Li, Li

APPLICANT: Caeman, Stacie

APPLICANT: Boidog, Ference

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby

FILE REFERENCE: 21402-251

CURRENT APPLICATION NUMBER: US/10/055,877

CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: 60/262,892

PRIOR FILING DATE: 2001-01-19

PRIOR APPLICATION NUMBER: 60/263,598

PRIOR FILING DATE: 2001-01-23

PRIOR APPLICATION NUMBER: 60/263,799

PRIOR FILING DATE: 2001-01-24

PRIOR APPLICATION NUMBER: 60/264,117

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 60/264,478

PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/263,351

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/272,870

PRIOR FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 60/275,990

Query Match

Best Local Similarity 59.5%, Score 979, DB 7, Length 320;

Matches 182, Conservative 55, Mismatches 67, Indels 2, Gaps 2;

Cy

Db

Cy

Db

Cy

Db

Cy

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Cy

Db

Sequence 933, App
Sequence 172, App

ALIGNMENTS

RESULT 2

US-10-055-877-336

Sequence 336, Application US/10055877

Publication No. US20050288241A1

GENERAL INFORMATION:

APPLICANT: Decristofaro, Marc

APPLICANT: Padigaru, Muralidhara

APPLICANT: Miller, Charles

APPLICANT: Tchernev, Velizar

APPLICANT: Zhong, Mei

APPLICANT: Anderson, David

APPLICANT: Ballinger, Robert

APPLICANT: Gerlach, Valerie

APPLICANT: Spytek, Kimberly

APPLICANT: Rattelli, Luca

APPLICANT: Kekuda, Ramesh

APPLICANT: Guo, Xiaojia

APPLICANT: Zethusen, Bryan

APPLICANT: Andrew, David

APPLICANT: Mezes, Peter

APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine

APPLICANT: Eileen, Andrew

APPLICANT: Wolenc, Adam

APPLICANT: Baumgartner, Jason

APPLICANT: Shimkets, Richard

APPLICANT: Gusev, Vladimir

APPLICANT: Vernet, Corinne

APPLICANT: Taupier Jr., Raymond

APPLICANT: Pena, Carol

APPLICANT: Shenoy, Suresh

APPLICANT: Li, Li

APPLICANT: Caeman, Stacie

APPLICANT: Boidog, Ference

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby

FILE REFERENCE: 21402-251

CURRENT APPLICATION NUMBER: US/10/055,877

CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: 60/262,892

PRIOR FILING DATE: 2001-01-19

PRIOR APPLICATION NUMBER: 60/263,598

PRIOR FILING DATE: 2001-01-23

PRIOR APPLICATION NUMBER: 60/263,799

PRIOR FILING DATE: 2001-01-24

PRIOR APPLICATION NUMBER: 60/264,117

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 60/264,478

PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/263,351

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/272,870

PRIOR FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: 60/275,990

Query Match

Best Local Similarity 59.5%, Score 979, DB 7, Length 320;

Matches 182, Conservative 55, Mismatches 67, Indels 2, Gaps 2;

Cy

Db

Cy

Db

Cy

Db

Cy

Db

Cy

Db

Cy

Db

Sequence 933, App
Sequence 172, App

ALIGNMENTS

RESULT 2

US-10-055-877-336

Sequence 336, Application US/10055877

Publication No. US20050288241A1

GENERAL INFORMATION:

APPLICANT: Decristofaro, Marc

APPLICANT: Padigaru, Muralidhara

APPLICANT: Miller, Charles

APPLICANT: Tchernev, Velizar

APPLICANT: Zhong, Mei

APPLICANT: Anderson, David

APPLICANT: Ballinger, Robert

APPLICANT: Gerlach, Valerie

APPLICANT: Spytek, Kimberly

APPLICANT: Rattelli, Luca

APPLICANT: Kekuda, Ramesh

APPLICANT: Guo, Xiaojia

APPLICANT: Zethusen, Bryan

APPLICANT: Andrew, David

APPLICANT: Mezes, Peter

APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine

APPLICANT: Eileen, Andrew

APPLICANT: Wolenc, Adam

APPLICANT: Baumgartner, Jason

APPLICANT: Shimkets, Richard

APPLICANT: Gusev, Vladimir

APPLICANT: Vernet, Corinne

APPLICANT: Taupier Jr., Raymond

APPLICANT: Pena, Carol

APPLICANT: Shenoy, Suresh

APPLICANT: Li, Li

APPLICANT: Caeman, Stacie

APPLICANT: Boidog, Ference

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby

FILE REFERENCE: 21402-251

CURRENT APPLICATION NUMBER: US/10

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P R I O R F I L I N G D A T E : 2001-03-14
P R I O R A P P L I C A T I O N N U M B E R : 60/275, 927
P R I O R F I L I N G D A T E : 2001-03-14
R E M A I N I N G P R I O R A P P L I C A T I O N d a t a r e m o v e d - S e e F i l e W r a p p e r o r P A L M .
N U M B E R O F S E Q I D N O S : 512
S O F T W A R E : P a t e n t i n V e r . 2.1
S E Q I D N O 336
L E N G T H : 329
T Y P E : P R I
O R G A N I S M : H o m o s a p i e n s
US-10-055-877-336

Query Match 55.0%; Score 892.5; DB 6; Length 329;
Best Local Similarity 52.5%; Pred. No.2.5e-74;
Matches 160; Conservative 63; Mismatches 81; Indels 1; Gaps 1

QY 6 NGNESSATYVFTLLGPGLEBAQFMFLAPLCSLLYLIALVAGNTLTITIVRTEHSHRPMTIF 65
DB 23 NSSSSVGAFTPLSGIPGERHIMISTILCPMTYLVISIGNCTILFIITRBSLHPMTLF 82
QY 66 LCMLSGIDILISTSSMPMTALIPWENSTTIQFDACLQIPAIHSUSGNESTVLLAMAFDR 125
DB 83 LSMALIDIGSLCTLPVLGIIPWVGABRI SHDACPAQLPFHICPSPIESSVILSMAPDR 142
QY 126 YVALCHPLRHAIVTLPFRVTKIGVAAVVRGALAMPVLFKOLPFCGNSNITSHSYCLHQ 185
DB 143 FVALCHPLHMYVILTMTVIGRIGLVLSGRSVALIPPLPMPKRFPYCGSPVLSHSHYCLHQ 202
QY 186 DVMGLACDDIRVNVVYGLIVIIISAIGDSLISFSYLLILKTVGLTREBAQ-KAFGTCV 244
DB 203 EVMGLACDDMKANSITGCMFVIVSTYIGDSLILPEYALILKTVLSIASRAERFKALNTCV 262
QY 245 SHVCAVPIFYVPFGLSNMRFPSKRKRDSPPLVILIANIYLVLPVLPNPIYGVYKTEIROR 304
DB 263 SHICAVLLFTYPMIGLSVIRHFGKQAPHLVQVVMGMFTLLPFPVNNPIYSVKTKQIRDR 322
QY 305 ILRLP 309
DB 323 VTHAF 327

RESULT 3
US-10-055-877-339
; Sequence 339, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decisofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelle, Luca
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zeehneen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Elsen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Verneer, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li

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APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
TITLE OR INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 339
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-339

Query Match      53.5%: Score 868.5; DB 6; Length 312;
Beet Local Similarity 53.6%; Pred. No. 3.7e-72;
Matches 163; Conservative 51; Mismatches 89; Indels 1; Gaps 1;

QY      8 N E S S A T F I L I G L P G L E A Q F W L A F P L C S I Y L I A V L G N L T T I Y I V R T E H S I H E B M Y I F L C 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      5 N V T H A P F L L T G I P G L S S W L S G P L C W Y A V A L G G N T V I L Q A V R P S L H E M Y I F L S 64

QY      68 M L S G I D I L I S T S M P K M L A I F W E N S T T I Q P D A C L I Q I P A I H S L S G M S T V L L A M A F D R Y 127
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      65 M L S P S D V A I S M A T P V I A R F C L A N R I T F D A C L I Q M F L I H F F S M S G I L L A M S F D R Y 124

QY      128 A I C H P L H A T Y L T P R T K I G V A A V R G A L M A D L P F I Q L P F C R N I I S H S Y C L H O D V 187
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      125 A I C P L P Y A V T L T T E V I A M G L G A A S F T L F P L P L I K R L P T C R S V I S H S Y C L H P D M 184

QY      188 M K L A D D I R V V V V G L I V I I S A I G L D S L I S F Y L L I L K T Y G - L T R E A Q A K A G T C V S H 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      185 M R L A C A D I S I N S I G L V L V S T F E M D L F F I L S T V L I R S M A T A S R E R K A L A N T C V S H 244

QY      247 V C A V F I F Y V P I G L S M W H R F S K R R D S P L P Y I L A N I Y L L V P E V L N P I Y V G T K E I R O R I L 306
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      245 I L A V L A F Y P M I G S T V H R F G K V P C Y I H V L M S V Y L F V P V L N P L I Y S A K T E I R A I F 304

QY      307 R L F H 310
      : : :
DB      305 R M F H 308

RESULT 4
US-11-190-188-8
; Sequence 8, Application US/11190188
; Publication No. US20060035331A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra

```

APPLICANT: YAO, Montique G.
APPLICANT: SHIH, Leo L.
APPLICANT: TRIBOUTEY, Catherine
APPLICANT: LU, Dyrung Aina M.
APPLICANT: YUE, Henry
APPLICANT: KHAN, Farrah A.
APPLICANT: POLICKI, Jennifer L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: YANG, Junning
APPLICANT: HARLAND, Lee
APPLICANT: WALSH, Roderick T.
APPLICANT: LO, Terence P.
APPLICANT: BOROWSKY, Mark L.
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0044 PCT
CURRENT APPLICATION NUMBER: US/11/190,188
CURRENT FILING DATE: 2005-07-27
PRIOR APPLICATION NUMBER: US/10/220,382
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 8
LENGTH: 315
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 7472361CD1
US-11-190-188-8

Query Match 51.0%; Score 827.5; DB 7; Length 315;

Best Local Similarity 49.8%; Pred. No. 2,1e-68; Matches 154; Conservative 64; Mismatches 90; Indels 1; Gaps 1;

QY 2 MVDNNGESSATYFLIGLPGLEAOWLAAPPLCSLYDAVAGNLTIIYVTERSHLEP 61
DB 1 MGDWNNSDAVAPFILRGFPGLEVYHWSLIFCLAYLVAFMGVNTILSVIMISSLIHQ 60
QY 62 MYTLCMLSGDILISTSSMPRLAIFPNSTTIOFDACLIQIPAIHLSGMSVTLAM 121
DB 61 MYEISITIAVNDLGMSLSTPLTMAVWLDAPEIOASACVQOLFPIHFTPLSSVLLAM 120
QY 122 AFDYVVAICHPRLAATVTLPRVTKIGVAAVVGAALMAPIPVFIKQDPFGSNLISHSY 181
DB 121 AFDYVVAICHPRLAATVTLPRVTKIGVAAVVGAALMAPIPVFIKQDPFGSNLISHSY 180
QY 182 CLHODVNLACDDIRVNVVYGLVYISAIGLSLISFSYLLIKTVLGL-TREAQAAAF 240
DB 181 CLHODVNLACDDIRVNVVYGLVYISAIGLSLISFSYLLIKTVLGL-TREAQAAAF 240
QY 241 GTCVSHVCAVPIFYVPPFGLSMWHRFSGRDSPLPVILANITYLVLPPLANTIVGVTKKE 300
DB 241 NTCSHICVAVIFVFPVIGVSMVHRFGHLSPIVHILMADIVLLPVLNPIVSVTRKQ 300
QY 301 IRRGILRLP 309
DB 301 IRRGILRLP 309
QY 301 IRRGILRLP 309
DB 301 IRRGILRLP 309

RESULT 5

US-10-511-538-70
Sequence 70, Application US/10511538
Publication No. US20060026700A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
FILE REFERENCE: 16U 200 PCT
CURRENT APPLICATION NUMBER: US/10/511,538
CURRENT FILING DATE: 2004-10-18
PRIOR APPLICATION NUMBER: US 60/372,669
PRIOR FILING DATE: 2002-04-16

PRIOR APPLICATION NUMBER: US 60/411,882
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US 60/424,336
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: US 60/374,823
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 60/376,558
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: US 60/381,366
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US 60/403,648
PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PatentIn version 3.1
SEQ ID NO 70
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-538-70

Query Match 50.1%; Score 812.5; DB 6; Length 314;

Best Local Similarity 50.7%; Pred. No. 4.9e-67; Matches 151; Conservative 59; Mismatches 87; Indels 1; Gaps 1;

QY 13 TYFLIGLPGLEAOWLAAPPLCSLYDAVAGNLTIIYVTERSHLEPMTYFLCMLSGI 72
DB 12 TAFLVGIPGLEHLMHISIPCLAYTLALGNCTLLITQADAAHBPVTLPLAMLAII 71
QY 73 DILISTSSMPRLAIFPNSTTIOFDACLIQIPAIHLSGMSVTLAMAFDRVVAICHP 132
DB 72 DLVIVSSALPRLAIFVFRDREINFACLAQMPFLHSFSTIESVLLAMAFDRVVAICHP 131
QY 133 LRHATVTLPRVTKIGVAAVVGAALMAPIPVFIKQDPFGSNLISHSYCLHODVNLAC 192
DB 132 LRHATVTLPRVTKIGVAAVVGAALMAPIPVFIKQDPFGSNLISHSYCLHODVNLAC 191
QY 193 DDIRVNVVYGLVYISAIGLSLISFSYLLIKTVLGL-TREAQAAAFGTCVSHVCAV 251
DB 192 GDTSENNITGVAVMFIYVLDLIVLSYFIQLQAVVLLASQEAHYKAFGTCVSHVCAV 251
QY 252 IFYVPPFGLSMWHRFSGRDSPLPVILANITYLVLPPLANTIVGVTKKEIRGILRLP 309
DB 252 AFYTVTVISSVMHVAHAAAPHVHILANFLLPFPVNPVITIVGKTKQIRESLIGVF 309

RESULT 6

US-10-055-877-335
Sequence 335, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Decristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchenev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Kaceli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zerhusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eileen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shimkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corinne

```

; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Caeman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining prior application data removed - See file wrapper or PAM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 335
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-877-335

Query Match          49.3%; Score 799.5; DB 6; Length 342;
Best Local Similarity 46.7%; Pred. No. 8,4e-66;
Matches 142; Conservative 72; Mismatches 89; Indels 1; Gaps 1;

QY 6 NNGESSATYVILGLGELERAOFWLAFPLCSYLIANLGNLTIIYVREHSIHEPMYIF 65
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 17 NNTIABLPILFGLNGIPGLKATQYWISIPCLLYVAASGNSMLLEVLCERSLHKPMYIF 76
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 66 LCMISGIDILISTSMKMLAIFWPNSTTIQPDACILQIFAIHSLSGSESTVLLAMAFDR 125
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 77 LSNLSATDLSLCTSTLTGTFWFEAREINLNCIOMFFLGFTMESGVLLAMAFDR 136
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 126 YVAICHLRAHYVLTLPRTVKIGVAAYVGAALMAPLVEFIKQLPFCRSNLSHSYCLHQ 185
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 137 FVAICPLRAHYVLTLPRTVKIGVAAYVGAALMAPLVEFIKQLPFCRSNLSHSYCLHQ 196
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 186 DWKCLACDDIRVAVVYVGLIYISAIIGDLSLISSTYLLIKTVLGL-TREAQAKAFGTCV 244
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 197 DLQLQCTDRIRINSIGLIPALSTGDCPCILISYLLIIRSYLSISASERRAFAFTCT 256
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 245 SHYCAVEIFVVPFGLSMVHRFSKRDSPLPVILANTYLLVPPVLANPIYGVKTEIKROR 304
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 257 SHISAVSIFVLPPLISLSVHRIGHSAPPFVHIIMANVFLIPVLANPIYGVKTEIKROR 316
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 305 ILRL 308
   | | | | |
DB 317 IIRV 320
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; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAB, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: YAO, Monique G.
; APPLICANT: SHIH, Leo L.
; APPLICANT: TRIBOULEY, Catherine
; APPLICANT: LU, Dnyung Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junming
; APPLICANT: HARLAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROMSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/11/190,188
; CURRENT FILING DATE: 2005-07-27
; PRIOR APPLICATION NUMBER: US/10/220,382
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 7472364CD1
US-11-190-188-10

Query Match          47.5%; Score 771; DB 7; Length 311;
Best Local Similarity 47.3%; Pred. No. 3.1e-63;
Matches 140; Conservative 71; Mismatches 83; Indels 2; Gaps 2;

QY 15 FILIGHGLEBAQFWLAFPLCSYLIANLGNLTIIYVREHSIHEPMYIFLCMLSGIDI 74
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 14 FLIGIIGLEBDFHMTWSGPFCSYVIVLGNATILLYIKVEQLRBRMFFLAILSTIDL 73
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 75 LISTSMKMLAIFWPNSTTIQPDACILQIFAIHSLSGSESTVLLAMAFDRYVAICHLPR 134
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 74 ALSATSVPRMIGIFWPDAREINYGACVACQMFLLHAFGMAEYVLLAMAFDRYVAICHLPR 133
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 135 HATVLTLPRTVKIGVAAYVGAALMAPLVEFIKQLPFCRSNLSHSYCLHQDWKCLACDD 194
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 134 YATILSVLVAVGSMCIVIRPVLTLPVYLLIYRLPCCQHIHSHSYCEMGIKLSGCGN 193
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 195 IRRNVVYGLIYISAIIGDLSLISSTYLLIKTVLGL-TREAQAKAFGTCVSHYCAVEIF 253
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 194 IIRNGIYGLFV-VSFPVLANVILGISVYVILRAVFLRPSHDAQKLSTGCAHYGVICVF 252
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 254 YVPFGLSMVHRFSKRDSPLPVILANTYLLVPPVLANPIYGVKTEIKRORILRLP 309
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 253 YIPSVSFLTRHFGHQIPGYIHIVANLVYLIIPPSINPIYGVRTYQIRBRVLYVF 308
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-10-055-877-338
; Sequence 338, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchertnev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
```

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APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Roteili, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zerhusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Bisen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 338
LENGTH: 321
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-338

```

Query Match	46.8%	Score 758.5	DB 6	Length 321
Best Local Similarity	45.2%	Pred. No. 4,4e-62		
Matches 140	Conservative 73	Identical 96	Indels 1	Gaps 1
QY	1	MMDPENGESSATYFILLGLPGLEBAQFWLAPLCLSYLIAVGNLTIIYVIRTEHSLSHE	60	
DB	7	MITSVSPSTSTNSPFLTLGFSGMEQOOWFMSIPFSISYAMVLLGNCMTVLWTPTPSLIHQ	66	
QY	61	PMYIFLCMSGLDIIISTSSMPKMLAIFWPNSTTQOPACLLQIPIAHSLSGMESTVLLA	120	
DB	67	PMFPLSLMALTLDCMGSLTYTVVLGILMRIIREISLDSGCIASQFPHGLSPWESSVLLT	126	
QY	121	MAFRRYAIACHPLRAATVTLTPRVTKIGVAANVRGALMAAPLPVATIKQLPFRKSNILSHS	180	
DB	127	MAFRRYAIAICPLKRSYSLTMSRIIKGTLIGTSRSPFFFTPTPICLKPFNYCHPHILSHS	186	
QY	181	YCLHQDVAKCACDDIRANVVYGLIYISAIGDSLIISESYLLIIKTVLGLTREAQAVXA	239	

Db 187 FCHODILRLACSDIRFNSYVAMLVICILLDAILILEPSYLLILKSVAVASQEBRHQ 246

QY 240 FGTCYSHCANVIFIVPVPICGSMVRFPGRKRSPLVPIANITLVLPPIANIPVYGVTK 259

Db 247 FQTCISHCANVAFVPIISLITMVRFGKHLSVAHVAILIGNITILFPPIMNPILYSVKTO 306

QY 300 EIRORILRLP 309

Db 307 QIHTRMLRLP 316

```

RESULT 9
US-11-190-188-9
; Sequence 9, Application US/11190188
; Publication No. US2006003531A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: YANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: YAO, Monique G.
; APPLICANT: SHIH, Leo L.
; APPLICANT: TRIBOUTIS, Catherine
; APPLICANT: LO, Dying Alma M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junning
; APPLICANT: HARLAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROMSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/11/190,188
; CURRENT FILING DATE: 2005-07-27
; PRIOR APPLICATION NUMBER: US/10/220,382
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7472363CD1
US-11-190-188-9

```

[illegible]

Db 305 FLTRFEHQIPGYHILVANKLIIIPSLNPIITGVATKQIREVLYVF 353

RESULT 10

US-11-124-367A-496
 ; Sequence 496, Application US/11124367A
 ; Publication No. US20060024700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: Hongjin Huang
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
 ; FILE REFERENCE: CU001519.ORD
 ; CURRENT APPLICATION NUMBER: US/11/124,367A
 ; CURRENT FILING DATE: 2005-05-09
 ; PRIOR APPLICATION NUMBER: US 60/568,846
 ; PRIOR FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: US 60/582,609
 ; PRIOR FILING DATE: 2004-06-25
 ; PRIOR APPLICATION NUMBER: US 60/599,554
 ; PRIOR FILING DATE: 2004-08-09
 ; NUMBER OF SEQ ID NOS: 34460
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 496
 ; LENGTH: 312
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-124-367A-496

Query Match 45.5%; Score 737.5; DB 7; Length 312;
 Best Local Similarity 44.4%; Pred. No. 3.6e-60;

Matches 133; Conservative 72; Mismatches 96; Indels 1; Gaps 1;

QY 7 GNESSATYFLILGPGLEBAQFWLAPLCSLYLAVLGNLTIIYIVRTSHLHEPMYIFL 66
 DB 2 GLNKSASTFQLTGPGKMKHWHIFPLAAYISILGSGTLPLINDNHLHEPMYIFL 61
 QY 67 CMISGIDILISTSMPPKMLAIFWNSSTTIQPDACLLQIFAIHSISGMESTVLLAMAFDRY 126
 DB 62 AMLAATDGLVLTPTVGLVLMDBREIGHGACFSQAYFHTLSVMEAGVLLAMAYDCR 121
 QY 127 VAICHPLRHATVLTLPRTKIGVAAVVRGALMAP-LPVFIKQLPFCRSNIIHSYCLHQ 186
 DB 122 ITTHNPKRTYSILNTWVMKIGRAVLTFRAGISIMPIVRLHWPYCRSHVLSHAFCLHQ 181
 QY 187 VMKLACDDIRVNVVYGLIYISAIGLDSLISPSYLLIKTVLGL-TREAQAKAFGTCVS 245
 DB 182 VITLACADITFNLPLPVVLPAMVLDPLFIIFPYIILIKTVGIGSGRAKALNTCVS 241
 QY 246 HVCAPVFIYVPIGLSVNRHRSKRDSPLPVILANITYLVPPVLPVIVGVKTEIRORI 305
 DB 242 HICCLVFFYVTVCLTPIHRFKGVPHVHITWSYIHFLPPFPNPIYSIKTKQIOSGI 301
 QY 306 LRLP 309
 DB 302 LRLP 305

RESULT 11

US-11-124-367A-514
 ; Sequence 514, Application US/11124367A
 ; Publication No. US20060024700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michele Cargill
 ; APPLICANT: Hongjin Huang
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with
 ; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
 ; FILE REFERENCE: CU001519.ORD
 ; CURRENT APPLICATION NUMBER: US/11/124,367A
 ; PRIOR APPLICATION NUMBER: US 60/568,846
 ; PRIOR FILING DATE: 2004-05-07

;; PRIOR APPLICATION NUMBER: US 60/582,609
 ;; PRIOR FILING DATE: 2004-06-25
 ;; PRIOR APPLICATION NUMBER: US 60/599,554
 ;; PRIOR FILING DATE: 2004-08-09
 ;; NUMBER OF SEQ ID NOS: 34460
 ;; SOFTWARE: FASTSEQ for Windows Version 4.0
 ;; SEQ ID NO 514
 ;; LENGTH: 312
 ;; TYPE: PRT
 ;; ORGANISM: Homo sapiens
 US-11-124-367A-514

Query Match 45.4%; Score 736.5; DB 7; Length 312;
 Best Local Similarity 45.8%; Pred. No. 4.4e-60;

Matches 142; Conservative 68; Mismatches 93; Indels 7; Gaps 4;

QY 8 NNESSATYFLILGPGLEBAQFWLAPLCSLYLAVLGNLTIIYIVRTSHLHEPMYIFLC 67
 DB 3 SSSSHPEFLTGFPGLEBAHWHISVFLPMYISILFGNGTLILLIKEDNHLHEPMYIFLA 62
 QY 68 MMSGIDILISTSMPPKMLAIFWNSSTTIQPDACLLQIFAIHSISGMESTVLLAMAFDRY 127
 DB 63 MLAATDGLVLTPTVGLVLMDBREIGHGACFSQAYFHTLSVMEAGVLLAMAYDRFI 122
 QY 128 AICHPLRHATVLTLPRTKIGVAAVVRGALMAP-LPVFIKQLPFCRSNIIHSYCLHQ 185
 DB 123 AICHPLRHATVLTLPRTKIGVAAVVRGALMAP-LPVFIKQLPFCRSNIIHSYCLHQ 180
 QY 186 DVKLACDDIRVNVVYGLIYISAIGLDSLISPSYLLIKTVLGL-TREAQAKAFGTCVS 244
 DB 181 DVKLACADITFNLPLPVVLPAMVLDPLFIIFPYIILIKTVLIGSGRAKALNTCV 240
 QY 245 SHVCAPVFIYVPIGLSVNRHRSKRDSPLPVILANITYLVPPVLPVIVGVKTEIRORI 304
 DB 241 SHICCVLVFVTVVGLIYISAIGLDSLISPSYLLIKTVLGL-TREAQAKAFGTCVS 300
 QY 305 ILRLPVATH 314
 DB 301 ILRLP--TTH 308

RESULT 12

US-10-055-877-123
 ; Sequence 123, Application US/10055877
 ; Publication No. US2005028241A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Decristofaro, Marc
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Tchermey, Velizar
 ; APPLICANT: Zhong, Wei
 ; APPLICANT: Anderson, David
 ; APPLICANT: Ballinger, Robert
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Ratelli, Luca
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Andrew, David
 ; APPLICANT: Mezes, Peter
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Bisen, Andrew
 ; APPLICANT: Wolenc, Adam
 ; APPLICANT: Baumgartner, Jason
 ; APPLICANT: Shimkets, Richard
 ; APPLICANT: Gusev, Vladimir
 ; APPLICANT: Verne, Corine
 ; APPLICANT: Raupler Jr., Raymond
 ; APPLICANT: Pena, Carol
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Li, Li


```

: APPLICANT: Ratelli, Luca
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Guo, Xiaojia
: APPLICANT: Zerhusen, Bryan
: APPLICANT: Andrew, David
: APPLICANT: Mezes, Peter
: APPLICANT: Paturajan, Meera
: APPLICANT: Burgess, Catherine
: APPLICANT: Eilen, Andrew
: APPLICANT: Molenc, Adam
: APPLICANT: Baumgartner, Jason
: APPLICANT: Shinkets, Richard
: APPLICANT: Gusev, Vladimir
: APPLICANT: Verneet, Corine
: APPLICANT: Taupier Jr., Raymond
: APPLICANT: Pena, Carol
: APPLICANT: Shenoy, Sureeh
: APPLICANT: Li, Li
: APPLICANT: Caeman, Stacie
: APPLICANT: Boldog, Ference
: TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
: FILE REFERENCE: 21402-251
: CURRENT APPLICATION NUMBER: US/10/055,877
: CURRENT FILING DATE: 2002-01-22
: PRIOR APPLICATION NUMBER: 60/262,892
: PRIOR FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: 60/263,598
: PRIOR FILING DATE: 2001-01-23
: PRIOR APPLICATION NUMBER: 60/263,799
: PRIOR FILING DATE: 2001-01-24
: PRIOR APPLICATION NUMBER: 60/264,117
: PRIOR FILING DATE: 2001-01-25
: PRIOR APPLICATION NUMBER: 60/264,139
: PRIOR FILING DATE: 2001-01-25
: PRIOR APPLICATION NUMBER: 60/264,478
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/263,351
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: 60/272,870
: PRIOR FILING DATE: 2001-03-02
: PRIOR APPLICATION NUMBER: 60/275,990
: PRIOR FILING DATE: 2001-03-14
: PRIOR APPLICATION NUMBER: 60/275,927
: PRIOR FILING DATE: 2001-03-14
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 512
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 222
: LENGTH: 318
: TYPE: PRT
: ORGANISM: Mus musculus
US-10-055-877-222

Query Match      29.3%; Score 475; DB 6; Length 318;
Best Local Similarity 35.7%; Pred. No. 3.8e-36;
Matches 114; Conservative 62; Mismatches 121; Indels 22; Gaps 7;

QY 8 NESSATVPIILGL---PGLERAOFLAPPLGSLYLIATVIGLTLTIYIRTHSHLEPYI 64
Db 5 NQITVTEVVLGLSHAPLKEKTFVL--IISMVILVILGSLVLSIILSHLHTPYF 61

QY 65 FLCLMSGIDILISTSMPEKMLAIFWFSSTTIQFDACLQIFAIHSLGMESTVLLAMAFD 124
Db 62 FLGLSLFLDICTYTSVPLVDGFLTPRKITSFSGCANQWMLSFAMGATECVLLGMMAFD 121

QY 125 RYVAICHPRLAATVLTLEPRVTIKIGVAANVRGALAMAPLVPFIKQLPFRSNILSHSYCLH 184
Db 122 RYVAICHPRLAATVLTLEPRVTIKIGVAANVRGALAMAPLVPFIKQLPFRSNILSHSYCLH 181

QY 185 QDWKLCACDDIRVAVVVGGLIVTISAIGDSLISFSYLLIKTVLGL-TREAQAKAPGTC 243
Db 182 LAVKLACADISINVISMGVANVIFLGVPLIFIVSYIFLSTILRIKIPSAGRKKAAPSTC 241
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QY 244 VSHVCAVFIFYPVPIGLSMVHFRPKRSDPLPV-----ILANIYLVPPVLPNIYVG 295
Db 242 SAHLTVVLIIFYGTLL---FMWGPKRSKD-PLGADKQDLADKLISLPLGLTRPMLNPIYS 297

QY 296 VKTKIRQRIILRPHVATH 314
Db 298 LRNDQVRAAVRNL---ASH 313

RESULT 17
US-10-055-877-326
: Sequence 326, Application US/10055877
: Publication No. US20050288241A1
: GENERAL INFORMATION:
: APPLICANT: Decristofaro, Marc
: APPLICANT: Padigaru, Muralidhara
: APPLICANT: Miller, Charles
: APPLICANT: Tchernev, Velizar
: APPLICANT: Zhong, Mei
: APPLICANT: Anderson, David
: APPLICANT: Ballinger, Robert
: APPLICANT: Gerlach, Valerie
: APPLICANT: Spytek, Kimberly
: APPLICANT: Ratelli, Luca
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Guo, Xiaojia
: APPLICANT: Zerhusen, Bryan
: APPLICANT: Andrew, David
: APPLICANT: Mezes, Peter
: APPLICANT: Paturajan, Meera
: APPLICANT: Burgess, Catherine
: APPLICANT: Eilen, Andrew
: APPLICANT: Molenc, Adam
: APPLICANT: Baumgartner, Jason
: APPLICANT: Shinkets, Richard
: APPLICANT: Gusev, Vladimir
: APPLICANT: Verneet, Corine
: APPLICANT: Taupier Jr., Raymond
: APPLICANT: Pena, Carol
: APPLICANT: Shenoy, Sureeh
: APPLICANT: Li, Li
: APPLICANT: Caeman, Stacie
: APPLICANT: Boldog, Ference
: TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
: FILE REFERENCE: 21402-251
: CURRENT APPLICATION NUMBER: US/10/055,877
: CURRENT FILING DATE: 2002-01-22
: PRIOR APPLICATION NUMBER: 60/262,892
: PRIOR FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: 60/263,598
: PRIOR FILING DATE: 2001-01-23
: PRIOR APPLICATION NUMBER: 60/263,799
: PRIOR FILING DATE: 2001-01-24
: PRIOR APPLICATION NUMBER: 60/264,117
: PRIOR FILING DATE: 2001-01-25
: PRIOR APPLICATION NUMBER: 60/264,139
: PRIOR FILING DATE: 2001-01-25
: PRIOR APPLICATION NUMBER: 60/264,478
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/263,351
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: 60/272,870
: PRIOR FILING DATE: 2001-03-02
: PRIOR APPLICATION NUMBER: 60/275,990
: PRIOR FILING DATE: 2001-03-14
: PRIOR APPLICATION NUMBER: 60/275,927
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 512
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 326
: LENGTH: 318
: TYPE: PRT
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ORGANISM: Mus musculus
US-10-055-877-326

Query Match 29.3%; Score 475; DB 6; Length 318;
Best Local Similarity 35.7%; Pred. No. 3.8e-36;
Matches 114; Conservative 62; Mismatches 121; Indels 22; Gaps 7;

QY 8 NESATYFILGL---PGLEBAQFWLAFLPCSLYLIVAGNLTIIYVTRSHLHEPMYI 64
DB 5 NQTVTFEVLILGSAHPLKTEKTFVL---ILSMVLVLGNGVILVLSIDSLHATPMYF 61
QY 65 FLCLMSGIDILISTSSMPKMLAIFMNSTTIOFDACLTQIFAIHSLSGMESTVLLAMAF 124
DB 62 FLGLSLFLDICTTSSVPLVLDGFLTRKTISSGCAVOMLSAMGATKCVLGMMAFD 121
QY 125 RYVAICPLRHATVLTLPRTKIGVAAVVRGALMALPVPFIKQLPFCRSNLSHSYCLH 184
DB 122 RYVAICPLRHATVLTLPRTKIGVAAVVRGALMALPVPFIKQLPFCRSNLSHSYCLH 181
QY 185 QDVWKLACDDIRVVNVVGLIVITSAIGLDSLISPSYLLIKTVGL-TREAQAKAFGC 243
DB 182 LAVLKACADISIVISVMGVANVIFLGVPVLFIFVSYIFILSTILRIPSAEGRKAFSTC 241
QY 244 VSHVCAVEIFVFPFGLSMVHRFSKRDSPLEV-----ILANITLVLPVLPNPIYVG 295
DB 242 SAHLTVITIIYGTIL---FMGKPKSKD-PLGADKODLADGLISLFGLTPLMLNPITIS 297
QY 296 VKTEIRORILRLPHVATH 314
DB 298 LRNDVKAAVRNL---ASH 313

RESULT 18
US-10-055-877-224
Sequence 224, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Decistofaro, Marc
APPLICANT: Padigaru, Murailidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mel
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Kekuda, Rameesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zernuoen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eissen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shimkets, Richard
APPLICANT: Guev, Vladimyr
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Caeman, Stacie
APPLICANT: Boldog, Ference
TITLE OR INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055, 877
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262, 892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263, 598

PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263, 799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264, 117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264, 139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264, 478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263, 351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272, 870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275, 990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275, 927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 224
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-224

Query Match 28.6%; Score 464; DB 6; Length 319;
Best Local Similarity 35.3%; Pred. No. 3.8e-35;
Matches 113; Conservative 64; Mismatches 111; Indels 32; Gaps 9;

QY 8 NESATYFILGL---PGLEBAQFWLAFLPCSLYLIVAGNLTIIYVTRSHLHEPMYI 63
DB 5 NETSPVGFVLLRSHAPBLKTEKTFVL---ILSMVLVLGNGVILVLSIDSLHATPMYF 61
QY 64 IFCLMSGIDILISTSSMPKMLAIFMNSTTIOFDACLTQIFAIHSLSGMESTVLLAMAF 123
DB 62 FLGLSLFLDICTTSSVPLVLDGFLTRKTISSGCAVOMLSAMGATKCVLGMMAFD 121
QY 124 DRYVAICPLRHATVLTLPRTKIGVAA-VVRGALMALPVPFIKQLPFCRSNLSHSYCLH 182
DB 122 DRYVAICPLRHATVLTLPRTKIGVAA-VVRGALMALPVPFIKQLPFCRSNLSHSYCLH 180
QY 183 LHQVWKLACDDIRVVNVVGLIVITSAIGLDSLISPSYLLIKTVGL-TREAQAKAFGC 241
DB 181 EILAVLKACADISIVISVMGVANVIFLGVPVLFIFVSYIFILSTILRIPSAEGRKAFSTC 240
QY 242 TCVSHVCAVEIFVFPFGLSMVHRFSKRDSPLEV-----PLPVITANIYLVLPV 288
DB 241 TCSAHLTVITIIYGTIL---LFMKGKPKSKD-SMGADKEDLSDKILPL-----FVGVTTPM 291
QY 289 LNPVYGVKTEIRORILRL 308
DB 292 LNPVYGVKTEIRORILRL 311

RESULT 19
US-11-190-188-12
Sequence 12, Application US/11190188
Publication No. US2006003531A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LAL, Preeti
APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Chandra
APPLICANT: YAO, Monique G.
APPLICANT: SHIH, Leo L.
APPLICANT: TRIBOULEY, Catherine
APPLICANT: LU, Dyrung Aina M.
APPLICANT: YOS, Henry
APPLICANT: KHAN, Farrah A.
APPLICANT: POLICKY, Jennifer L.
APPLICANT: AU-YOUNG, Janice
APPLICANT: YANG, Junming

```
; APPLICANT: HARIAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROMSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/11/190,188
; PRIOR FILING DATE: 2005-07-27
; PRIOR APPLICATION NUMBER: US/10/220,382
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7472435CD1
US-11-190-188-12
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Query Match 28.6%; Score 464; DB 7; Length 319;
Best Local Similarity 35.3%; Pred. No. 3.8e-35;
Matches 113; Conservative 64; Mismatches 111; Indels 32; Gaps 9;
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QY 8 NESAATY-FILIGL---PGLBAGFWLAFPLCSLYLVIAVGNLTIIYIVRTSHSLHEPMY 63
DB 5 NESTVWGFVLRLRSANHELEKTFVY---ILMLTVLLGNGVILVITIIIDSRILHTPMY 61
QY 64 IFLCMLSGIDILISTSMRPMKLAIFWNSSTTIQFDACLQIFAIHSLSGMESTVLLANAF 123
DB 62 FFLGNLSTFDICFTTSVPLVLDSELTPOETISFSAQVQMALSPAMAGTECLLSMAAF 121
QY 124 DRYVAICHPRLHATVLTTPRTYKIGVAA-VVRGALMAPLPVFIQQLPFCRSNLSHSYC 182
DB 122 DRYVAICHPRLHATVLTTPRTYKIGVAA-VVRGALMAPLPVFIQQLPFCRSNLSHSYC 180
QY 183 LHQVWMLKACDDIRVVVYGLIVISAIGLDSLISFYLILKTVLGL-TREAQAKAF 241
DB 181 EILAVLKACADISINVISMEVTNVIPLGVPLFISFVITITILIPSAEGKAYFS 240
QY 242 TCVSHVCAVFIYVYFPIGLSMVHRFSKRRDS-----PLPYILANIYLLVPPV 288
DB 241 TCSAHLTVVIVFYGT---LFWYGGKPKSGKDSGADKEDLSDKLPL-----FYGVVTPM 291
QY 289 LNPVYGVKTEIKRRIIRL 308
DB 292 LNPVYSLRNKDVKAARRL 311
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RESULT 20

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US-10-511-538-21
; Sequence 21, Application US/10511538
; Publication No. US20060026700A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
; FILE REFERENCE: 16U 200 PCT
; CURRENT APPLICATION NUMBER: US/10/511,538
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: US 60/372,669
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,882
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/424,336
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/374,823
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/376,558
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 60/381,366
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; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/403,648
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-538-21
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Query Match 28.5%; Score 463; DB 6; Length 319;
Best Local Similarity 33.5%; Pred. No. 4.7e-35;
Matches 106; Conservative 63; Mismatches 133; Indels 14; Gaps 5;
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QY 6 NNESSATYFPIILGLPGLBAGFWLAFPLCSLYLVIAVGNLTIIYIVRTSHSLHEPMYIF 65
DB 7 SGNQVWTFPLFSMPFAHNGGLIFPIPLIITGFIILGMLIMFVIQGMALHTPLXPF 66
QY 66 LCMLSGIDILISTSMRPMKLAIFWNSSTTIQFDACLQIFAIHSLSGMESTVLLANAFDR 125
DB 67 ISVLSFLEICVTTTIRKMLSCLSISBQKISVAGCLIQWTFHSLGITESCVLTMAIDR 126
QY 126 YVAICHPRLHATVLTTPRTYKIGVAAVVRGALMAPLPVFIQQLPFCRSNLSHSYCLHQ 185
DB 127 YVAICHPRLHATVLTTPRTYKIGVAAVVRGALMAPLPVFIQQLPFCRSNLSHSYCLHQ 186
QY 186 DVMGLACDDIRVVVYGLIVISAIGLDSLISF-----SYLILKTVLGL-TREAQAKA 239
DB 187 PVLSLACTDT-----FLVIVDVAIHAAEIVASVLVLTALSTIRITIIYILGMSHSGHNKA 240
QY 240 FGTCVSHVCAVFIYVYFPIGLSMVHRFSKRRDSPLPYILANIYLLVPPVNPVYGVKTX 299
DB 241 FSTQANH-AVFLFPGSVAV-WYLRFSATYGVWDAIAVTFILAPFFNPVILYSLKNK 298
QY 300 EIRORIIRLPHVATHA 315
DB 299 DMKEAIRGLPHYOKRA 314
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Search completed: March 9, 2006, 08:44:24
Job time : 23 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 9, 2006, 08:25:34 ; Search time 40 Seconds
(without alignments)
764.923 Million cell updates/sec

Title: US-10-001-469A-2866

Perfect score: 1622
Sequence: 1 MMWDPMGNBSATYFILGL.....KRIQRILRLPHYVATNASEP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	552	34.0	292	2 A60547	hypothetical prote
2	473.5	29.2	313	2 E45774	odorant receptor 8
3	453	27.9	307	2 S29710	olfactory receptor
4	440	27.1	312	2 A46247	olfactory receptor
5	434.5	26.8	312	2 I23701	olfactory receptor
6	431.5	26.6	310	2 E23701	olfactory receptor
7	430.5	26.5	319	2 UC5624	olfactory receptor
8	429.5	26.5	312	2 S29708	olfactory receptor
9	428	26.4	328	2 G45774	odorant receptor 2
10	427.5	26.4	314	2 S20572	olfactory receptor
11	425.5	26.2	314	2 A37286	olfactory receptor
12	423.5	26.1	314	2 S29707	olfactory receptor
13	420.5	25.9	321	2 H45774	odorant receptor 3
14	418.5	25.8	305	2 S29711	olfactory factor 0
15	418.5	25.8	309	1 S51356	olfactory receptor
16	413	25.5	312	2 A48413	probable olfactory
17	411	25.3	160	2 S58066	probable olfactory
18	411	25.3	344	2 I45774	odorant receptor 1
19	407.5	25.1	311	2 UC5200	chemoreceptor 1B33
20	407	25.1	313	2 S20571	olfactory receptor
21	404.5	24.9	312	2 G23701	olfactory receptor
22	404.5	24.9	313	2 B23701	olfactory receptor
23	402.5	24.8	311	2 G23701	olfactory receptor
24	402.5	24.8	314	2 H23701	olfactory receptor
25	401	24.7	317	2 F45774	odorant receptor 4
26	396.5	24.4	316	2 A57069	olfactory receptor
27	395.5	24.4	328	2 D45774	odorant receptor 3
28	395.5	24.4	328	2 A45774	odorant receptor 3
29	393.5	24.3	328	2 B45774	odorant receptor 3

30	390.5	24.1	320	2 S20573	olfactory receptor
31	388.5	24.0	312	2 A46750	olfactory receptor
32	386.5	23.8	304	2 S29709	olfactory receptor
33	384.5	23.7	315	2 UC5836	olfactory receptor
34	383.5	23.6	328	2 G45774	odorant receptor 3
35	383	23.6	333	2 A23701	olfactory receptor
36	379.5	23.4	327	2 F23701	olfactory receptor
37	375	23.1	317	2 D23701	olfactory receptor
38	371.5	22.9	315	2 UC4658	olfactory receptor
39	370	22.8	318	2 UC5201	chemoreceptor 1B64
40	366	22.6	318	2 UC5202	G protein-coupled
41	313.5	19.3	234	2 S29000	odorant receptor (
42	310.5	19.1	222	2 B40745	olfactory receptor
43	303.5	18.7	264	2 PC4369	olfactory receptor
44	289.5	17.8	234	2 S28939	G protein-coupled
45	285.5	17.6	222	2 D40745	odorant receptor (
46	280.5	17.3	234	2 S28938	G protein-coupled
47	277	17.1	225	2 S29001	olfactory receptor
48	261.5	16.1	232	2 S29001	G protein-coupled
49	259.5	16.0	216	2 I38474	olfactory receptor
50	254.5	15.7	216	2 I38470	olfactory receptor
51	254.5	15.7	216	2 I38480	olfactory receptor
52	249.5	15.4	216	2 I38479	olfactory receptor
53	239.5	14.8	222	2 C40745	odorant receptor (
54	235.5	14.5	135	2 PN0530	G protein-coupled
55	232.5	14.3	216	2 I38472	olfactory receptor
56	232.5	14.3	216	2 I38464	olfactory receptor
57	227.5	14.0	185	2 S28936	olfactory receptor
58	226	13.9	215	2 I38473	olfactory receptor
59	223.5	13.8	216	2 I38482	olfactory receptor
60	221.5	13.7	216	2 I38483	olfactory receptor
61	220.5	13.6	216	2 I38476	olfactory receptor
62	216.5	13.3	216	2 I38461	olfactory receptor
63	212.5	13.1	216	2 I38477	olfactory receptor
64	211.5	13.0	168	2 S28937	G protein-coupled
65	210.5	13.0	163	2 S58028	probable olfactory
66	194.5	12.0	157	2 S58000	probable olfactory
67	187.5	11.6	332	2 A57055	melanocortin recep
68	187	11.5	320	2 S17177	probable G protein
69	184.5	11.4	318	2 S38511	adenosine receptor
70	182.5	11.3	352	2 UB0296	thyrotropin releas
71	182	11.2	143	2 S58006	probable olfactory
72	181.5	11.2	161	2 A40745	odorant receptor (
73	181.5	11.2	317	2 S29204	melanotropin recep
74	181	11.2	165	2 I38471	olfactory receptor
75	180	11.1	320	2 A46152	Ad adenosine recep
76	180	11.1	323	2 S43850	melanocortin 3 rec
77	178	11.0	143	2 S58071	probable olfactory
78	177	10.9	154	2 S58069	probable olfactory
79	176.5	10.9	317	2 S45708	MGR receptor - bov
80	176	10.9	325	2 UN0764	melanocortin recep
81	174.5	10.8	157	2 S58068	probable olfactory
82	174	10.7	325	2 UC5592	melanocortin 5 rec
83	173.5	10.7	584	2 UC7809	bulfafrin recepto
84	173	10.7	427	2 S50150	gastric CCK-A rece
85	172.5	10.6	157	2 S58033	probable olfactory
86	172.5	10.6	360	2 B46647	melanocortin recep
87	172	10.6	314	2 S71420	melanocortin 1 rec
88	171	10.6	314	2 S71420	melanocortin 1 rec
89	170.5	10.5	157	2 S58019	probable olfactory
90	169.5	10.5	337	2 S68678	adenosine receptor
91	169	10.4	324	2 S55302	Al(1) adenosine rec
92	168.5	10.4	157	2 S57939	probable olfactory
93	168.5	10.4	157	2 S58035	probable olfactory
94	168	10.4	325	2 UC2193	melanocortin recep
95	167.5	10.3	157	2 S58026	probable olfactory
96	167.5	10.3	158	2 S58016	probable olfactory
97	167	10.3	362	2 PN0694	angiotensin II rec
98	166.5	10.3	157	2 S58023	probable olfactory
99	164.5	10.1	156	2 S58072	probable olfactory
100	164.5	10.1	157	2 S58030	probable olfactory


```
Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992
```

A>Title: Spatial pattern of receptor expression in the olfactory epithelium.

A:Reference number: A46247; MUID:93028384; PMID:1384038

A:Accession: A46247

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-312 <NEF>

A:Cross-references: UNIPROT:P23275; UNIPARC:UPI0000029735; GB:M64005; NID:g200153; PIDN:A>Note: sequence extracted from NCBI database (NCBIF:115362)

C:Superfamily: olfactory receptor OR1A

```
Query Match          27.1%, Score 440; DB 2; Length 312;  
Best Local Similarity 34.6%, Pred. No. 1e-30;  
Matches 113; Conservative 65; Mismatches 123; Indels 26; Gaps 11;
```

OY 1 MMVDPNNGESSATYFIILIGL--FGLEBAQFWMLAPPLCSLYLVANGLTIIVRTSHS 57
| | | | | : | : | : | : | : | : | : | : | : | : |
1 MEVDSN---SSSGFFILMGVSDHPHLETTFPAV--IIASYLTLTVGNLTITILLSRLDAR 54

Dy 58 LHREMTYFLCMLGSDIDLITSSTSMRKALAFWNSSTIQPACLLQTPAHISLSGMESTV 117
| | | | | : | : | : | : | : | : | : | : | : | : |
55 LHTPMYFPFLNSTSLDLAFITTSVPQLMKLMGPDKTISYGCVCTQLVFVLMLATETCL 114

OY 118 LLMAAPRYVAICGPLRHAATVLTPRVTKIGVAAV--VRGAALAAPIPVFKOLPFGRSN 175
| | | | | : | : | : | : | : | : | : | : | : | : |
115 LVVAAPFRIVAACGPLRHMYTMVN--PRLC-WGLAISWLGGAGSVISTFTLQLPFCGR 172

Dy 176 ILSSHYSCLADQVMKACDDIRVN--VVYGLIIVISAIGLDLISFSYLLIKTVLG-T 232
| | | | | : | : | : | : | : | : | : | : | : | : |
173 KVDNFLCEVPAMIKLACODTSLNEAVLNVCOTFPFTVAVSVITV--SYCFIAQAQVMKIRS 230

OY 233 REAQAKAFGCIVSHVCAVIPTYPVFIGLSMHRP---SKRDSELPVTIANITYLVPPVL 289
| | | | | : | : | : | : | : | : | : | : | : | : |
231 VEGRRKAFNCTVSLLVVVFIFYG----SAIYYGLLPKASSNOQGKPSLFYSVTPMV 285

OY 290 NPITYGVKTKEIRORILRLFVATHAS 316
| | | : | : | : | : | : | : | : | : | : | : |
Db 286 NFLTYLRNKVKCALGRHLGKGGRGAS 312

RESULT 5

I23701

Olfactory receptor I14 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C:Accession: I23701

R:Buck, L.; Axel, R.
Cell 65, 175-187, 1991

A>Title: A novel multigene family may encode odorant receptors: a molecular basis for o

A:Reference number: A23701; MUID:91191556; PMID:1840504

A:Accession: I23701

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-312 <BCU>

A:Cross-references: UNIPROT:P23273; UNIPARC:UPI000004157F; GB:M64391; NID:g205843; PIDN:C:Superfamily: olfactory receptor OR1A

C:Keywords: G protein-coupled receptor; transmembrane protein

```
Query Match          26.8%, Score 434.5; DB 2; Length 312;  
Best Local Similarity 33.5%, Pred. NO. 3e-30;  
Matches 105; Conservative 64; Mismatches 119; Indels 25; Gaps 7;
```

OY 8 NESSATYFIILIGLGBEBAQFWMLAPPLCSLYLVANGLTIIVRTSHSLHEPYITLC 67
| | | : | : | : | : | : | : | : | : | : | : |
5 NGTILIRILLGLRIPISEYHLLFYALPLAMLTITILGSLLIIVRLDSHLMRPYIFLS 64

Dy 68 MLSCGDILISTSMPKMLAIWFNSSTIQPACLQTPAHISLSGMESTVLLMAAFDRIV 127
| | | : | : | : | : | : | : | : | : | : | : |
65 NLSPSDICLFSSVTWPKLQNMQSQVPSISYTGCTQLTLYFEVWFQDMESFLLVVNAVDRYV 124

OY 128 AICPLRHAATVLTLPVTKIGVAHV-----RGAAALAAPVPVFKOLPFGRSNLISHSX 181
| | | | | : | : | : | : | : | : | : | : | : | : |
125 AICPLPKRTITMS---TKPCASLVLLIMLTMTTHALTHTL-LIARSFGCKNVITHRF 178

QY 182 CLHQDVKKACDDIRVN-----VVYGLIVIIISAIIGDSLISFSYLLIKTVLGL--TREA 235
 Db 179 CDISALAKTCSDSIDYVNEIMYIIYIGGLIIII-----PFLIYWSYIRIFPSILKFPSTQD 233
 QY 236 QAKAFGTCVSHVCAVFIFYVPFGLSMVHRFSKRSDSPVLIIANTYLLVPPVLNPVYG 295
 Db 234 IYKVFSTCGSHLSVTLTFYGTIFGIYLCF--SGNNSTYKAIAMAMMYTVVTPMLNPFYIS 291
 QY 296 VKTEIRKRIIRL 308
 Db 292 LRNRDMKRALLRV 304
 RESULT 6
 E23701
 olfactory receptor 13 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
 C:Accession: E23701
 R:Buck, L.; Axel, R.
 Cell 65, 175-187, 1991
 A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A:Reference number: A23701; MUID:91191556; PMID:1840504
 A:Accession: E23701
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-310 <BUC>
 C:Cross-references: UNIPROT:P23269; UNIPARC:UP10000041F7B; GB:M64365; NID:9205831; PIDN:
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; transmembrane protein
 Query Match 26.6%; Score 431.5; DB 2; Length 310;
 Best Local Similarity 33.2%; Pred. No. 5, 4e-30;
 Matches 102; Conservative 71; Mismatches 121; Indels 13; Gaps 7;
 QY 8 NESAATYFPIILGLPGLSEAQC--FWLAFPLCSILYLAIVLGNLTIIYVTRHSLHEPMYIF 65
 Db 3 NQRTITGLLGLPIPEBHQHFLVALFLV--MYLFTILNLIIIVQLDSQLTPLYLF 60
 QY 66 LCHTSGDIIISTSMPPMLAFWNSTTIQDACLQIPATHSLSGMESTVLLAMADR 125
 Db 61 LSNISFSLCFSSVTMPKLQNMRSQDTSIPYGCIAQTYPFVWFGDMSEFLVAMAYDR 120
 QY 126 YVAICHPRLHATVTLTPVTKIGVA--AVVGAALMAFLPVFIKQLPFCRSNLSHSYC 182
 Db 121 YVAICFPLHYSIMS-PKLCCTGLVLLMWLTSHAMHTL--LAAKLSFCENNVVLANPFC 177
 QY 183 LHQDMKLACDDIRVVVYGLIIVISAIIGDSLISFSYLLIKTVLGL--TREQAQAFG 241
 Db 178 DLFLVTKLAKGSDTYINELMIFIMSTLIIIPFLIYWSYARIISSILKVPSTQDICVFS 237
 QY 242 TCVSHVCAVFIFYVPFGLSMVHRFSKRSDSPVLIIANTYLLVPPVLNPVYGVKTEI 301
 Db 238 TCGSHLSVTSIFYGTIFGIYLCF--AGNNSTYKEMAMMYTVVTPMLNPFYISLRNRM 295
 QY 302 KRIIRL 308
 Db 296 KRALIRV 302
 RESULT 7
 JC5624
 olfactory receptor HTRCR92 - human
 C:Species: Homo sapiens (man)
 C:Date: 14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
 C:Accession: JC5624; 858003
 R:Vanderhaeghen, P.; Schumann, S.; Vassart, G.; Parmentier, M.
 Biochem. Biophys. Res. Commun. 237, 283-287, 1997
 A:Title: Molecular cloning and chromosomal mapping of olfactory receptor genes expressed
 A:Reference number: JC5624; MUID:97415789; PMID:9268701
 A:Contents: Testis
 A:Accession: JC5624

RESULT 10

520572
Olfactory receptor - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S20572
R/Parmentier, M.; Libert, F.; Schuurmans, S.; Schiffrmann, S.; Lefort, A.; Begerick, D.;
Nature 355, 453-455, 1992
A/Title: Expression of members of the putative olfactory receptor gene family in mammals
A/Reference number: S20571; MUID:92131132; PMID:1370859
A/Accession: S20572
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-314 <BUC>
A/Cross-references: UNIPROT:P30953; UNIPARC:UPI0000041BB6; EMBL:X64994; NID:g32085; PIDN:
C/Superfamily: olfactory receptor OR14
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.4%; Score 427.5; DB 2; Length 314;

Best Local Similarity 34.5%; Pred. No. 1.2e-29;
Matches 108; Conservative 64; Mismatches 120; Indels 21; Gaps 8;

QY 8 NBSATYFIIIGLPGLEBAQ--FWLAFPLCSLYLAVGNLTIIYVREHSLHEPMYIFLC 67
DB 5 NQVISDFLLGLPIQEPQOMCYALFLAMYLTLTGLNLTIIYIRLDSHLHTPMYIFLS 64
QY 68 MLGSGIDILISTSNPKMLAIFWNSSTTIQPDACLIQIFAHLSGMSSTVLLAMAAPDRYV 127
DB 65 NLSPSDFLCSFSSVTIPKLLQNMNQDPSIPYADCTQWYFLLPFDLSFLVMAAYDRYV 124
QY 128 AICPPLHATYLTLPRTYKGV--AVRGALMPLPFTIKOLPFCRSNLSHSYCLH 184
DB 125 AICPPL-HYTAIMSPMLCLALVALSWLTTFHAMLT--LMARLCFCADVVIPIHPCDM 181
QY 185 QDVWKLACDDIRVN----VYGLIIVIIISAIGLDSLISPSYLLIKTVLGL-TRBAQAK 238
DB 182 SALMLKAPSDRVNEMVIFPIGSLIVY----PPLLSGVARIIVSILKVPSSKICK 236
QY 239 AFGTGVSHVCAVFIYVPFGLSMVHRFSKRDSPL-PVILANIYLLVPPVLANPIYGVK 297
DB 237 AFSICGSHLSVSLFYGVTVGLYLC--SSANSTLTMDTVWAMMYTVTPMLNPFITSLR 293
QY 298 TKRIRQRIILRL 310
DB 294 NRDMKGLSRVTH 306

RESULT 11

A37286
Olfactory receptor 115 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C/Accession: A37286
R/Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A/Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A/Reference number: A23701; MUID:91191556; PMID:1840504
A/Accession: A37286
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-314 <BUC>
A/Cross-references: UNIPROT:P23274; UNIPARC:UPI0000040A93; GB:M64392; NID:g205845; PIDN:
C/Superfamily: olfactory receptor OR14
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.2%; Score 425.5; DB 2; Length 314;

Best Local Similarity 33.2%; Pred. No. 1.8e-29;
Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;

QY 8 NBSATYFIIIGLPGLEBAQ--FWLAFPLCSLYLAVGNLTIIYVREHSLHEPMYIF 65
DB 5 NQVISDFLLGLPIQEPQOMCYALFLAMYLTLTGLNLTIIYIRLDSHLHTPMYIFLS 64

DB 5 NQVISDFLLGLPIQEPQOMCYALFLAMYLTLTGLNLTIIYIRLDSHLHTPMYIF 62

QY 66 LCMISGIDILISTSNPKMLAIFWNSSTTIQPDACLIQIFAHLSGMSSTVLLAMAAPDR 125

DB 63 LSNLSPSDFLCSFSSVTIPKLLQNMNQDPSIPYAGCTQLTFYLYFADLSFLVMAAYDR 122

QY 126 YVAILCHPLRHATYLTLPRTYKGVAAVVRGAALM--APL-PVPIKOLPFCRSNLSHSY 181

DB 123 YVAILCHPLRHATYLTLPRTYKGVAAVVRGAALM--APL-PVPIKOLPFCRSNLSHSY 178

QY 182 CLHODVWKLACDDIRVN----VYGLIIVIIISAIGLDSLISPSYLLIKTVLGL-TRBA 235

DB 179 CDISPLKLSGSDTHVEMLVIFWAGLVIVIPV----LIYSAVAVASILKVPSSGIRG 233

QY 236 QAKAFGTGVSHVCAVFIYVPFGLSMVHRFSKRDSPL-PVILANIYLLVPPVLANPIYVG 295

DB 234 IHKIFSTCGSHLSVSLFYGVTVGLYLC--SSANSTLTMDTVWAMMYTVTPMLNPFITSLR 291

QY 296 TKRIRQRIILRL 308

DB 292 LRNDMKGLSRVTH 304

RESULT 12

S29707
Olfactory receptor OR5 - rat

C/Species: Rattus norvegicus (Norway rat)
C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004

C/Accession: S29707; B37286
R/Raming, K.; Krieger, J.; Stroctmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer,

Nature 361, 353-356, 1993
A/Title: Cloning and expression of odorant receptors.

A/Reference number: S29707; MUID:93149273; PMID:7678922

A/Accession: S29707

A/Molecule type: mRNA

A/Residues: 1-314 <RAM>

A/Cross-references: UNIPROT:Q04059; UNIPARC:UPI0000042031

R/Buck, L.; Axel, R.

Cell 65, 175-187, 1991

A/Title: A novel multigene family may encode odorant receptors: a molecular basis for od

A/Reference number: A23701; MUID:91191556; PMID:1840504

A/Accession: B37286

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 193-236 <BUC>

A/Cross-references: UNIPARC:UPI000008403; GB:M64375; NID:g205811; PIDN:AAA41738.1; PID:5

C/Keywords: G protein-coupled receptor; membrane protein

Query Match 26.1%; Score 423.5; DB 2; Length 314;

Best Local Similarity 34.4%; Pred. No. 2.7e-29;
Matches 104; Conservative 64; Mismatches 119; Indels 15; Gaps 7;

QY 8 NBSATYFIIIGLPGLEBAQ--FWLAFPLCSLYLAVGNLTIIYVREHSLHEPMYIF 65
DB 5 NQVISDFLLGLPIQEPQOMCYALFLAMYLTLTGLNLTIIYIRLDSHLHTPMYIF 62
QY 66 LCMISGIDILISTSNPKMLAIFWNSSTTIQPDACLIQIFAHLSGMSSTVLLAMAAPDR 125
DB 63 LSNLSPSDFLCSFSSVTIPKLLQNMNQDPSIPYAGCTQLTFYLYFADLSFLVMAAYDR 122
QY 126 YVAILCHPLRHATYLTLPRTYKGVAAVVRGAALM--APL-PVPIKOLPFCRSNLSHSY 181
DB 123 YVAILCHPLRHATYLTLPRTYKGVAAVVRGAALM--APL-PVPIKOLPFCRSNLSHSY 178
QY 182 CLHODVWKLACDDIRVN----VYGLIIVIIISAIGLDSLISPSYLLIKTVLGL-TRBAQAKAF 240
DB 179 CDISPLKLSGSDTHVEMLVIFWAGLVIVIPV----LIYSAVAVASILKVPSSGIRG 233
QY 241 GTCVSHVCAVFIYVPFGLSMVHRFSKRDSPL-PVILANIYLLVPPVLANPIYGVKTKS 300
DB 239 SSCGSHLSVSLFYGVTVGLYLC--SSANSTLTMDTVWAMMYTVTPMLNPFITSLRND 296
QY 301 IR 302

Db 297 IK 298

RESULT 13

H45774

odorant receptor 3 - channel catfish

C:Species: Ictalurus punctatus (channel catfish)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: H45774

R:Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.

Cell 72, 657-666, 1993

A:Title: The family of genes encoding odorant receptors in the channel catfish.

A:Reference number: H45774; MUID:93201590; PMID:791654

A:Accession: H45774

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-321 <NGA>

A:Cross-references: UNIPROT:O9PSJ2; UNIPARC:UPI0000042021

A:Experimental source: olfactory epithelium

A:Note: sequence extracted from NCBI backbone (NCBI:127745)

C:Superfamily: olfactory receptor OR14

C:Keywords: olfaction; transmembrane protein

Query Match 25.9%; Score 420.5; DB 2; Length 321;

Best Local Similarity 32.4%; Pred. No. 5,1e-29;

Matches 101; Conservative 69; Mismatches 127; Indels 15; Gaps 6;

Query 10 SGAIV-----FILGLPGLERAGFWLAPLCSLYLIAVGNLTIIYIVRTHSLHEPMYI 64

Db 14 TNATFIRPSTFYITGLVNIIPAKYYLF-LCFVYVTFEGNSFVIGTITLARSLHTAKYI 72

Query 65 FLGMSGIDILISTSMRPMALIFWNSSTTIOFDACLIQIPAIHSLSGMESTVLLAMAPD 124

Db 73 AVFNIALSDLCGSSALIKRLDMLFENQISYEKLSNMFVYCFMLOCTTLALAYD 132

Query 125 RYVALICHLRATVLTLPRTVTKIGAAVAVRGALMAPLPVFIKQLPFCRSNITLSHSLH 184

Db 133 RLAIICVYLRAHYATTKAAMFIIIGAMVVLVSVAVALITRLSFCRSTTVVSFCDH 192

Query 185 QDVWKLACDDIRVNVVGLIIVISAGLDSLLISSTYLLT-----LKTVLGLTREQAQAF 240

Db 193 GPIYKLCNDNTVINSIMQVCTATLLYPLLLIILASVYICGPAQOKIHGV---EQVAKM 249

Query 241 GTCVSHVCAVPIFYVPFIFGLSVHRSKRDSPLVLIANTIIYLVPLVNPVGVKTKK 300

Db 250 KTCVSHLILVAMFPIIISVTV-ALTTRIDTNIINITALTQTTPMLNPITITLKTBE 308

Query 301 IRQRIILRF-HV 311

Db 309 VMQAIKLLYKH 320

RESULT 14

S29711

olfactory factor OR37 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998

C:Accession: S29711

R:Ramling, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubic, S.; Baumstark, C.; Breez

Nature 361, 353-356, 1993

A:Title: Cloning and expression of odorant receptors.

A:Reference number: S29707; MUID:93149273; PMID:1678922

A:Accession: S29711

A:Molecule type: mRNA

A:Residues: 1-305 <RAM>

A:Cross-references: UNIPARC:UPI000003PF7B

C:Superfamily: olfactory receptor OR14

Query Match 25.8%; Score 418.5; DB 2; Length 305;

Best Local Similarity 32.5%; Pred. No. 7,2e-29;

Matches 100; Conservative 62; Mismatches 115; Indels 31; Gaps 5;

Query 16 ILIGLPGLERAGFWLAPLCSLYLIAVGNLTIIYIVRTHSLHEPMYIPLCMLSGIDIL 75

Db 1 LILIGLGPKEIRILYFVILVMVLVIRHNGVLLIASIPDSHLTPMVPFLGNSFLDIC 60

Query 76 ISTSMRPMALIFWNSSTTIOFDACLIQIPAIHSLSGMESTVLLAMAPDVVALCHPLRH 135

Db 61 YTTSSVSTVLSLISKRNISFSGCTVQMFVGFWMGSTECILGLMAMPDRVALCNPLRY 120

Query 136 ATVALTLRVRTKI-----GVAIVRGALMAPLPVFIKQLPFCRSNITLSHSLHODV 187

Db 121 SVMSKSVYVMSMASWFSGGINSVQTSIAM-----RLPFCGNVNIHFCEVLAV 172

Query 188 MKLACDDIRVNVVGLIIVISAGLDSLLISFSTYLLIKTVLGL-TREQAQAFGTCVSH 246

Db 173 LKLA CADISINIVTMVISNMAFLVLPILLIFPSYVLLITLRNNSASGRKAPSTCSAH 232

Query 247 VCAVFIYVPFIFGSMHRSKRDSPL-----PVLIANTIIYLVPLVNPVGVK 297

Db 233 LTVVVIYFGTIFSM-----YAKPKSODLTGKDKFQTSDKIISLPYGVVTPMLNPITISLR 287

Query 298 TKRIRORI 305

Db 288 MKDVKAIV 295

RESULT 15

S51356

olfactory receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S51356; S47014

R:Gat, U.; Nekrasova, E.; Lancel, D.; Nacochin, M.

Eur. J. Biochem. 225, 1157-1168, 1994

A:Title: Olfactory receptor proteins. Expression, characterization and partial purificati

A:Reference number: S51356; MUID:95045546; PMID:7957207

A:Accession: S51356

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-309 <GAT>

A:Cross-references: UNIPROT:O63395; UNIPARC:UPI00000405D8; EMBL:X80671; NID:9517365; PID

R:Gat, U.; Nekrasova, E.; Lancel, D.; Nacochin, M.

submitted to the EMBL Data Library, July 1994

A:Description: Olfactory receptor proteins: expression, characterization and partial puri

A:Reference number: S47014

A:Accession: S47014

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-309 <GAT>

A:Cross-references: UNIPARC:UPI00000405D8; EMBL:X80671; NID:9517365; PIDN:CA56697.1; PI

C:Superfamily: olfactory receptor OR14

Query Match 25.8%; Score 418.5; DB 1; Length 309;

Best Local Similarity 33.0%; Pred. No. 7,3e-29;

Matches 104; Conservative 63; Mismatches 119; Indels 29; Gaps 8;

Query 7 GNESSATYFIIIGLPGLERAGFWLAPLCSLYLIAVGNLTIIYIVRTHSLHEPMYIPL 66

Db 5 GNSHAAVVVFIYVGLTKQPELLPLFPLFVIVYVTVGNLGMILLIVSLPHRPMYVFL 64

Query 67 CMLSGIDILISTSMRPMALIFWNSSTTIOFDACLIQIPAIHSLSGMESTVLLAMADRY 126

Db 65 SLSFVFLCVSTVITPKLVFLCKQNFIVSBCMAOFFFAIPVVEGYLLTVMADRY 124

Query 127 VAICHLRATVLTLPRTVTKIGV-----AAVVRGALMAPLPVFIKQLPFCRSNITL 177

Db 125 VALCRPLLVNTIKS-SHICSLVAVAPSLGFSVAVHTSAM-----NLSFCKSYII 175

Query 178 SHSYCLHODWKLACDDIRVNVVGLIIVISAGLDSLLISFSTYLLIKTVLGL-TRE 234

Db 176 SHYFCDALPLKLKACSNTHNEL--LIFITGANTVPTLAVASVYFIFESIRIRNSE 233

Query 235 AQAATFGTCVSHVCAVPIFY--VPFGLSVHRSKRDSPLPVLIANTIIYLVPLVNP 292

Db 235 AQAATFGTCVSHVCAVPIFY--VPFGLSVHRSKRDSPLPVLIANTIIYLVPLVNP 292

Db 234 GRKAPOTCSHLMVAVGIFGSIPTMYLKSSSSNSLEQEK----VSSVFYTYVPMNLPL 289

QY 293 VYGVKTKETIRORILR 307

Db 290 IYSLRNQVKKALGR 304

RESULT 16

A48413 probable olfactory receptor OLFR1 - human

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A48413

R/Schumann, S.; Muscatelli, F.; Miot, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.

Cytogenet. Cell Genet. 63, 200-204, 1993

A/Title: The OLFR1 gene encoding the HGM07B putative olfactory receptor maps to the 17p

A/Reference number: A48413; MUID:93251832; PMID:8097991

A/Accession: A48413

A/Molecule type: DNA

A/Residues: 1-312 <SCH>

A/Cross-references: UNIPROT:P34982; UNIPARC:UP10000041B06; EMBL:X65857; NID:g425220; PIR

A/Note: sequence extracted from NCBI backbone (NCBIN:131483, NCBIIP:131485)

C/Genetics:

A/Genes: GDB:OLFR1

A/Cross-references: GDB:136274; OMIM:164342

A/Map position: 17p13-17p12

C/Superfamily: olfactory receptor OR14

C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

P/26-49/Domain: transmembrane #status predicted <TM1>

P/57-79/Domain: transmembrane #status predicted <TM2>

P/101-120/Domain: transmembrane #status predicted <TM3>

P/140-164/Domain: transmembrane #status predicted <TM4>

P/197-219/Domain: transmembrane #status predicted <TM5>

P/237-255/Domain: transmembrane #status predicted <TM6>

P/272-291/Domain: transmembrane #status predicted <TM7>

P/5/Binding site: carboxylate (asn) (covalent) #status predicted

P/137,232,290/Binding site: phosphate (Ser) (covalent) #status predicted

P/312/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 25.5%; Score 413; DB 2; Length 312;

Best Local Similarity 30.6%; Pred. No. 2.2e-28;

Matches 97; Conservative 81; Mismatches 107; Indels 32; Gaps 12;

Db 7 GNESSATYFLLIGL---PGLBAQFPLAPLCSYLAVGNLTIIYIVRTSHLSHPMY 63

Db 4 GNOSBGEFLLGSSSEPEOQILFMM---FLSMYLVTVGNVILIALISDSRLTPVY 60

QY 64 IPCMISGIDILISTSMRPMALFWMNSTTIOPDACLIOIFAHSLSGMESTVLLMAF 123

Db 61 PFLANISFTDLFPYVNTIIPKMLVNLQSHNKAISYAGCLTQLYFLVSLVALDNLTLAVMAY 120

QY 124 DRVVALCHPLRHATVTLPR---VTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLS 178

Db 121 DRVVALICPLHYTAMS-PKLCILLLSCLWLVLYG-LIHTL-LMTVTPFGSKIH 175

QY 179 HSYCLHODVKKACDDIRVN---VVYGLVIISAGLDSLLISFSYLLIKTVLGLTRE 234

Db 176 YIFCEMVLRLMCSNIQINHTVLIATGCFILIPFG---FVLIISYVLIIRAILRIPSV 231

QY 235 AQK-KARGTCVSHVCAPIFY--VPFGLSMVHRFSKRDSPPLVILANIYLLVPLVLP 291

Db 232 SKKYKASTCASHGASLSLFGTLCMYLKLPLHTYS-KOSVATV---MVAVTPPMNP 286

QY 292 IVYGVKTKETIRORILR 308

Db 287 FIVSLRNQVKKALGR 303

RESULT 17

S58066

probable olfactory receptor tpcr33 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C/Accession: S58066

R/Vanderhaeghen, P.; Schumann, S.; Vassart, G.; Parmentier, M.

submitted to the EMBL Data Library, July 1995

A/Description: Male germ cells from several mammalian species express a specific reperto

A/Reference number: S57995

A/Accession: S58066

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-160 <VAN>

A/Cross-references: UNIPROT:Q62336; UNIPARC:UP10000042009; EMBL:X89685; NID:g902668; PIR

C/Superfamily: olfactory receptor OR14

Query Match

Best Local Similarity

Matches

Db 129

QY 1

Db 188

QY 61

Db 246

QY 120

Db 145774

QY 145774

Db 1

QY 1

Db 1

QY 1

Db 1

QY 1

Db 1

QY 1

Db 1

QY 1

Db 1

QY 1

Db 1

QY 1

Db 1

QY 1

Db 1

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 9, 2006, 08:22:14 ; Search time 231 Seconds
(without alignments)
971.247 Million cell updates/sec

Title: US-10-001-469a-2866

Perfect score: 1622

Sequence: 1 MWDPNGNSATYFILIG.....KEIRQRRLRFVATASRP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1619	99.8	318	2	061F93_HUMAN
2	1614	99.5	317	1	051R13_HUMAN
3	1614	99.5	317	1	051R13_HUMAN
4	1612	99.4	318	2	066X57_HUMAN
5	1512	93.2	317	2	08VG27_MOUSE
6	1498	92.4	317	2	05MD65_RAT
7	1113	68.6	223	2	06SNE2_PPRIM
8	985	60.7	320	2	08VBV9_MOUSE
9	979	60.4	320	1	051R2_HUMAN
10	979	60.4	320	1	061F94_HUMAN
11	977	60.2	320	1	051R2_RAT
12	967.5	59.6	322	2	08VP03_MOUSE
13	937.5	57.8	324	1	051D1_HUMAN
14	914.5	56.4	315	2	08VH05_MOUSE
15	901.5	55.6	312	2	08VH11_MOUSE
16	892.5	55.0	314	1	051G2_HUMAN
17	892.5	55.0	314	1	061F87_HUMAN
18	877	54.1	313	2	08VH17_MOUSE
19	875.5	54.0	314	2	08VG26_MOUSE
20	873.5	53.9	314	2	08VG22_MOUSE
21	873.5	53.9	318	2	08VG23_MOUSE
22	868.5	53.5	312	1	05112_HUMAN
23	868.5	53.5	312	2	08VH01_HUMAN
24	862.5	53.2	317	2	08VH01_MOUSE
25	859.5	53.0	319	2	08VH01_MOUSE
26	857.5	52.9	314	2	08VH01_MOUSE
27	857.5	52.9	319	2	08VH01_MOUSE
28	854	52.7	319	2	08VH04_MOUSE
29	852.5	52.6	317	2	08VH04_MOUSE
30	852	52.5	317	2	08VH04_MOUSE
31	846.5	52.2	319	2	08VH09_MOUSE

32	844.5	52.1	314	2	07TR52_MOUSE
33	843	52.0	326	2	07TR56_MOUSE
34	841.5	51.9	321	1	052P1_HUMAN
35	838.5	51.7	312	2	08VG46_MOUSE
36	835.5	51.5	314	2	08VH15_MOUSE
37	835	51.5	330	2	08VP07_MOUSE
38	834	51.4	316	2	08VGX8_MOUSE
39	833.5	51.4	317	2	08VGX8_MOUSE
40	831.5	51.3	316	2	07TR55_MOUSE
41	831.5	51.3	317	2	08VG09_MOUSE
42	831.5	51.3	319	2	08VG16_MOUSE
43	831.5	51.3	327	2	08VH28_MOUSE
44	831	51.2	312	2	08VH12_MOUSE
45	829	51.1	311	2	07TR53_MOUSE
46	829	51.1	316	2	08VH16_MOUSE
47	827.5	51.0	314	2	08VG85_MOUSE
48	827.5	51.0	315	1	05111_HUMAN
49	827.5	51.0	315	2	061F85_HUMAN
50	826	50.9	316	2	08VG79_MOUSE
51	825.5	50.9	315	2	08VG75_MOUSE
52	824	50.8	317	2	08NGK5_HUMAN
53	823.5	50.8	321	1	051G1_HUMAN
54	823.5	50.8	321	2	07TRP8_MOUSE
55	823.5	50.8	329	2	08VGX9_MOUSE
56	822.5	50.7	316	2	08VG20_MOUSE
57	818.5	50.5	312	2	08VP02_MOUSE
58	817	50.4	313	1	051A4_HUMAN
59	816.5	50.3	316	2	07TR17_MOUSE
60	816	50.3	319	2	09YH55_CHICK
61	815	50.2	321	2	061F86_HUMAN
62	814.5	50.2	313	2	08VG14_MOUSE
63	814	50.2	315	2	08VG23_MOUSE
64	812.5	50.1	314	1	052K2_HUMAN
65	812.5	50.1	314	2	061F84_HUMAN
66	811.5	50.0	314	2	08VH21_MOUSE
67	811	50.0	321	1	052N4_HUMAN
68	811	50.0	321	2	061F77_HUMAN
69	809.5	49.9	315	2	07TRQ2_MOUSE
70	809.5	49.9	321	2	08VH20_MOUSE
71	808.5	49.8	314	1	052K1_HUMAN
72	808.5	49.8	314	2	061F85_HUMAN
73	808.5	49.8	317	2	06W053_MOUSE
74	807.5	49.8	315	2	07TRQ3_MOUSE
75	806.5	49.7	314	1	05111_HUMAN
76	806.5	49.7	314	2	061F93_HUMAN
77	806	49.7	312	2	08VG42_MOUSE
78	805.5	49.7	314	2	07TRR0_MOUSE
79	805.5	49.7	321	2	08VH19_MOUSE
80	803.5	49.5	314	2	07TRR7_MOUSE
81	803	49.5	326	2	09WV09_MOUSE
82	802	49.4	325	2	08VG15_MOUSE
83	801.5	49.4	312	1	051A7_HUMAN
84	801.5	49.4	312	2	061F88_HUMAN
85	799.5	49.3	330	1	051P1_HUMAN
86	799.5	49.3	342	2	061F11_HUMAN
87	799	49.3	302	1	051H1_HUMAN
88	799	49.3	302	2	061F13_HUMAN
89	799	49.3	312	1	052E4_HUMAN
90	799	49.3	312	2	061F80_HUMAN
91	799	49.3	313	2	07TRR8_MOUSE
92	799	49.3	317	2	08VH13_MOUSE
93	797.5	49.2	322	2	08VG05_MOUSE
94	796	49.1	316	2	09B005_MOUSE
95	795	49.0	311	2	07TRR4_MOUSE
96	794	49.0	318	2	08VH14_MOUSE
97	794	49.0	318	2	08VG13_MOUSE
98	794	49.0	328	2	06W055_MOUSE
99	793.5	48.9	314	2	08VG11_MOUSE
100	793.5	48.9	316	2	08VH03_MOUSE

ALIGNMENTS

RESULT 1
 Q6IFP93_HUMAN PRELIMINARY; PRT; 318 AA.
 ID Q6IFP93_HUMAN
 AC Q6IFP93
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Olfactory receptor OR11-15.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 CC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA PubMed:14983052; DOI=10.1073/pnas.0307882100;
 RA Mainic B., Godfrey P.A., Buck L.B.;
 RT "The human olfactory receptor gene family."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).
 CC -1- MSCELANOUS: The sequence shown here is derived from an
 EMBL/Genbank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK004369; DA04767.1; -; Genomic_DNA.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0004874; F:Olfactory receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007166; P:G-protein coupled receptor protein signaln. .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000725; Olfact_receptor.
 DR PANTHER; PTHR11398; Olfact_receptor; 1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00245; GPCRHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
 KW Receptor.
 SQ SEQUENCE 318 AA; 35402 MW; 9412125346584865 CRC64;
 Query Match 99.8%; Score 1619; DB 2; Length 318;
 Blast Local Similarity 99.7%; Pred. No. 1,1e-113;
 Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVDPNGSSATYFLLGLPGLBEAQFWLAFPLCLSLVLAIVGLTIYVTRTHSLH 60
 DB 1 MMVDPNGSSATYFLLGLPGLBEAQFWLAFPLCLSLVLAIVGLTIYVTRTHSLH 60
 QY 61 PMYIFLCMLSGIDILISTSSMPKMLAIWFNSTTIQPDACLIQFAHISGMESTVLLA 120
 DB 61 PMYIFLCMLSGIDILISTSSMPKMLAIWFNSTTIQPDACLIQFAHISGMESTVLLA 120
 QY 121 MAPFRYVAICPLRHATVTLPRYTKIGVAVVRAAAMAPLPVPIKLPFCRSNIISSH 180
 DB 121 MAPFRYVAICPLRHATVTLPRYTKIGVAVVRAAAMAPLPVPIKLPFCRSNIISSH 180
 QY 121 MAPFRYVAICPLRHATVTLPRYTKIGVAVVRAAAMAPLPVPIKLPFCRSNIISSH 180
 DB 121 MAPFRYVAICPLRHATVTLPRYTKIGVAVVRAAAMAPLPVPIKLPFCRSNIISSH 180
 QY 181 YCLHODVWKLACDDIRVAVVGLIYIISAGISLISISFSYLLIKTYLGLTREQAQAF 240
 DB 181 YCLHODVWKLACDDIRVAVVGLIYIISAGISLISISFSYLLIKTYLGLTREQAQAF 240
 QY 241 GTCVSHVCAVPIFYVPFGLSMVHRFSGRDSPPLVLIANTYLLVPPVLANPIVGVKTXE 300
 DB 241 GTCVSHVCAVPIFYVPFGLSMVHRFSGRDSPPLVLIANTYLLVPPVLANPIVGVKTXE 300
 QY 301 IRRRIILRLFHVATASEP 318
 DB 301 IRRRIILRLFHVATASEP 318
 QY 301 IRRRIILRLFHVATASEP 318
 DB 301 IRRRIILRLFHVATASEP 318
 RESULT 2
 OS1E1_HUMAN STANDARD; PRT; 317 AA.
 AC Q8TCS6;
 DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Olfactory receptor 51E1.
 DR
 GN Name=OR51E1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes."
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RN
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marisica K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Guncat P.H.,
 RA Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Hyers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
 RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -1- DATABASE: NMR=Human Olfactory Receptor Data Explorer
 (HORDS);
 WWW="http://bip.wetzmann.ac.il/cgi-bin/HORDS/showGene.pl?key=symbol&value=OR51E1";
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AB065787; BAC06006.1; -; Genomic_DNA.
 CC EMBL; BC022401; AA022401.1; -; mRNA.
 CC Ensembl; ENSG00000180785; Homo sapiens.
 CC HGNC; HGNC:15194; OR51E1.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000725; Olfact_receptor.
 DR PANTHER; PTHR11398; Olfact_receptor; 1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00245; GPCRHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Multi-gene family; Olfaction;
 KW Receptor; Sensory transduction; Transducer; Transmembrane.
 FT TOPO_DOM 1 27
 FT TRANSMEM 28 48 1 (Potential).
 FT TOPO_DOM 49 56
 FT TRANSMEM 57 77 2 (Potential).
 FT TOPO_DOM 78 101
 FT TRANSMEM 102 122 3 (Potential).


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PT TOPO DOM 123 141 Cytoplasmic (Potential).
PT TRANSMEM 142 162 4 (Potential).
PT TOPO DOM 163 198 Extracellular (Potential).
PT TRANSMEM 199 219 5 (Potential).
PT TOPO DOM 220 238 Cytoplasmic (Potential).
PT TRANSMEM 239 259 6 (Potential).
PT TOPO DOM 260 274 Extracellular (Potential).
PT TRANSMEM 275 295 7 (Potential).
PT TOPO DOM 296 317 Cytoplasmic (Potential).
PT CARBOHYD 7 N-linked (GLCNAC. . .) (Potential).
PT CARBOHYD 90 90 N-linked (GLCNAC. . .) (Potential).
PT DISULFID 99 191 By similarity.
SQ SEQUENCE 317 AA; 35271 MW; 8C7293AA7FBCA95C CRC64;

Query Match 99.5%; Score 1614; DB 1; Length 317;
Best Local Similarity 99.7%; Pred. No. 2.6e-113;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MVDPNGESSATYFILGLPGLBEAQFWLAFPLCSLYLVAVGNLTIIYIVRTHSHLP 61
DB 1 MVDPNGESSATYFILGLPGLBEAQFWLAFPLCSLYLVAVGNLTIIYIVRTHSHLP 60
QY 62 MYIFLCMLSGIDILISTSSMPKMLAFWFSSTTIQFACLLQIFAHSLSGMESTVLLAM 121
DB 61 MYIFLCMLSGIDILISTSSMPKMLAFWFSSTTIQFACLLQIFAHSLSGMESTVLLAM 120
QY 122 AFDRYVAICPLRHATVLTLPRTYKIGVAAVVRGALMALPVPFIKQLPFCRSNIIISHSY 181
DB 121 AFDRYVAICPLRHATVLTLPRTYKIGVAAVVRGALMALPVPFIKQLPFCRSNIIISHSY 180
QY 182 CLHQDVWKLACDDIRVVVYGLVITISAGLDSLLISFSYLLIKTVLGLTREAOAKAFG 241
DB 181 CLHQDVWKLACDDIRVVVYGLVITISAGLDSLLISFSYLLIKTVLGLTREAOAKAFG 240
QY 242 TCVSHVCAVFIFFVPPFGLSMVHRFSKRKRDSPPLVILANTYLLVPPVLANPIVGVKTKEI 301
DB 241 TCVSHVCAVFIFFVPPFGLSMVHRFSKRKRDSPPLVILANTYLLVPPVLANPIVGVKTKEI 300
QY 302 RORILRLFHVATNASEP 318
DB 301 RORILRLFHVATNASEP 317

RESULT 3
Q5S4P5_HUMAN PRELIMINARY; PRT; 317 AA.
ID Q5S4P5_HUMAN PRELIMINARY; PRT; 317 AA.
AC Q5S4P5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Prostate overexpressed G protein-coupled receptor.
GN Name=POGR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
OC NCBI_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RL Wang J., Wang J., Cai Y., Ittmann M., Liu M.;
RT "POGR, a prostate-overexpressed G protein-coupled receptor is a
RT sensitive biomarker for human prostate cancer.",
RT Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY75731; AAV54110.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; P:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR000725; Olfact_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00245; OLFACTORXR.
DR PRINTS; PR00245; OLFACTORXR.
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DR PROSITE; PS00237; G PROTEIN RECP_F1_1; UNKNOWN_1.
DR PROSITE; PSS0262; G_PROTEIN_RECP_F1_2; 1.
DR KW RECEPTOR.
SQ SEQUENCE 317 AA; 35271 MW; 8C7293AA7FBCA95C CRC64;

Query Match 99.5%; Score 1614; DB 2; Length 317;
Best Local Similarity 99.7%; Pred. No. 2.6e-113;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MVDPNGESSATYFILGLPGLBEAQFWLAFPLCSLYLVAVGNLTIIYIVRTHSHLP 61
DB 1 MVDPNGESSATYFILGLPGLBEAQFWLAFPLCSLYLVAVGNLTIIYIVRTHSHLP 60
QY 62 MYIFLCMLSGIDILISTSSMPKMLAFWFSSTTIQFACLLQIFAHSLSGMESTVLLAM 121
DB 61 MYIFLCMLSGIDILISTSSMPKMLAFWFSSTTIQFACLLQIFAHSLSGMESTVLLAM 120
QY 122 AFDRYVAICPLRHATVLTLPRTYKIGVAAVVRGALMALPVPFIKQLPFCRSNIIISHSY 181
DB 121 AFDRYVAICPLRHATVLTLPRTYKIGVAAVVRGALMALPVPFIKQLPFCRSNIIISHSY 180
QY 182 CLHQDVWKLACDDIRVVVYGLVITISAGLDSLLISFSYLLIKTVLGLTREAOAKAFG 241
DB 181 CLHQDVWKLACDDIRVVVYGLVITISAGLDSLLISFSYLLIKTVLGLTREAOAKAFG 240
QY 242 TCVSHVCAVFIFFVPPFGLSMVHRFSKRKRDSPPLVILANTYLLVPPVLANPIVGVKTKEI 301
DB 241 TCVSHVCAVFIFFVPPFGLSMVHRFSKRKRDSPPLVILANTYLLVPPVLANPIVGVKTKEI 300
QY 302 RORILRLFHVATNASEP 318
DB 301 RORILRLFHVATNASEP 317

RESULT 4
Q6KX57_HUMAN PRELIMINARY; PRT; 318 AA.
ID Q6KX57_HUMAN PRELIMINARY; PRT; 318 AA.
AC Q6KX57;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Dresden-G-protein-coupled receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
OC NCBI_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RL TISSUE=Prostate;
RC PubMed=1531197; DOI=10.1016/j.birc.2004.07.106;
RA Weigle B., Fuessel S., Ebner R., Temme A., Schmitz M., Schwind S.,
RA Klesling A., Rieger M.A., Meye A., Bachmann M., Wirth M.P.,
RA Rieber B.P.;
RT "D-GPCR: a novel putative G protein-coupled receptor overexpressed in
RT prostate cancer and prostate.",
RT Biochem. Biophys. Res. Commun. 322:239-249 (2004).
RL EMBL; AY698056; AAU07996.1; -; mRNA.
DR EMBL; ENSG00000180785; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; P:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00245; OLFACTORXR.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PSS0262; G_PROTEIN_RECP_F1_2; 1.
DR PROSITE; PSS0262; G_PROTEIN_RECP_F1_2; 1.
DR KW RECEPTOR.
```

SO SEQUENCE 318 AA; 35386 MW; 94121253D324B65 CRC64;
 Query Match 99.4%; Score 1612; DB 2; Length 318;
 Best Local Similarity 99.4%; Pred. No. 3.7e-113;
 Matches 316; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MMVDPNGSSATYFIIIGLPLESAQFWLAFPLCSLYLIANGLNLTIIYVTRTHSHL 60
 DB 1 MMVDPNGSSATYFIIIGLPLESAQFWLAFPLCSLYLIANGLNLTIIYVTRTHSHL 60
 QY 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTIIQPDACILQIPAHISLSGMESTVLLA 120
 DB 61 PMYIFLCMSGIDILISTSSMPKMLAFWNSSTIIQPDACILQIPAHISLSGMESTVLLA 120
 QY 121 MAPRYYAICHPRLHATVLTLPVTKIGVAAVGGAALMAPLPVPIKLPFCRSNIIISHS 180
 DB 121 MAPRYYAICHPRLHATVLTLPVTKIGVAAVGGAALMAPLPVPIKLPFCRSNIIISHS 180
 QY 181 YCLHODVWKLACDDIRVNVVYGLIVYISAGLDSILISFSYLLIKTVLGLTREAOAKAF 240
 DB 181 YCLHODVWKLACDDIRVNVVYGLIVYISAGLDSILISFSYLLIKTVLGLTREAOAKAF 240
 QY 241 GTCVSHVCAVPIFYVPPIGLSMVHRFSKRDSPLPVIIANIYLLVPPVLANPIYGVKTK 300
 DB 241 GTCVSHVCAVPIFYVPPIGLSMVHRFSKRDSPLPVIIANIYLLVPPVLANPIYGVKTK 300
 QY 301 IRORIILRFHVATHASEP 318
 DB 301 IRORIILRFHVATHASEP 318

RESULT 5
 OSMD65 RAT PRELIMINARY; PRT; 317 AA.

AC OSMD65; 1
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
 DE Olfactory receptor MOR18-1 (Olfactory receptor Olfr558) (Prostate overexpressed G protein coupled receptor).
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21676863; PubMed=11802173;
 RA Zhang X., Firestein S.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 5:124-133(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
 RA Young J.M., Friedman C., Williams E.M., Rose J.A., Tomnes-Priddy L., Trask B.J.;
 RT "Different evolutionary processes shaped the mouse and human olfactory receptor gene families."
 RL Hum. Mol. Genet. 11:535-546(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
 RA Young J.M., Shykand B.M., Lane R.P., Tomnes-Priddy L., Rose J.A., Walker M., Williams E.M., Trask B.J.;
 RT "Olfactory receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels."
 RL Genome Biol. 4:R71-R71(2003).

RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RA Wang J., Wang J., Itmann M., Liu M.;
 RT "PCR, an olfactory G-protein coupled receptor, is overexpressed in human prostate and prostate cancers."
 RL Submitted (NOV-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY072993; AL60656.1; -; Genomic DNA.
 DR EMBL; AY317671; AAP1050.1; -; mRNA.
 DR EMBL; AY834217; AA97880.1; -; mRNA.
 DR EMBL; ENSMUSG0000049016; Mus musculus.
 DR MGI; MGI:3030392; Olfr558.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004964; F:olfactory receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007185; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodan.
 DR InterPro; IPR000725; Olfact_receptor.
 DR PANTHER; PTHR11398; Olfact_receptor; 1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRODOPN.
 DR PRINTS; PR00245; OLFACTORR.
 DR PROSITE; PS00237; G_PROTEIN_RECER_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECER_F1_2; 1.
 KW Receptor.
 SO SEQUENCE 317 AA; 35464 MW; 5A0B59E229852534 CRC64;

Query Match 93.2%; Score 1512; DB 2; Length 317;
 Best Local Similarity 93.4%; Pred. No. 1.2e-105;
 Matches 295; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 MWDNGSSATYFIIIGLPLESAQFWLAFPLCSLYLIANGLNLTIIYVTRTHSHL 61
 DB 1 MWDNGSSATYFIIIGLPLESAQFWLAFPLCSLYLIANGLNLTIIYVTRTHSHL 60
 QY 62 MYIFLCMSGIDILISTSSMPKMLAFWNSSTIIQPDACILQIPAHISLSGMESTVLLA 121
 DB 62 MYIFLCMSGIDILISTSSMPKMLAFWNSSTIIQPDACILQIPAHISLSGMESTVLLA 120
 QY 122 AFDRYYAICHPRLHATVLTLPVTKIGVAAVGGAALMAPLPVPIKLPFCRSNIIISHS 181
 DB 122 AFDRYYAICHPRLHATVLTLPVTKIGVAAVGGAALMAPLPVPIKLPFCRSNIIISHS 180
 QY 181 YCLHODVWKLACDDIRVNVVYGLIVYISAGLDSILISFSYLLIKTVLGLTREAOAKAF 240
 DB 181 YCLHODVWKLACDDIRVNVVYGLIVYISAGLDSILISFSYLLIKTVLGLTREAOAKAF 240
 QY 242 TCVSHVCAVPIFYVPPIGLSMVHRFSKRDSPLPVIIANIYLLVPPVLANPIYGVKTK 301
 DB 242 TCVSHVCAVPIFYVPPIGLSMVHRFSKRDSPLPVIIANIYLLVPPVLANPIYGVKTK 300
 QY 302 RORILRFHVATHASE 317
 DB 302 RORILRFHVATHASE 316
 RESULT 6
 OSMD65 RAT PRELIMINARY; PRT; 317 AA.
 AC OSMD65; 1
 DT 01-FEB-2005 (Tremblrel. 29, Created)
 DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)
 DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
 DE Prostate overexpressed G protein coupled receptor.
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Murinae; Rattus.
 NC NCBI_TaxID=10116;

[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=BN;
RA Meng J., Wang J., Ittmann M., Liu M.;
RT "POGR, an olfactory G-protein coupled receptor, is overexpressed in
human prostate and prostate cancer.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY834218; AAV97881.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
DR Receptor.
SQ SEQUENCE 317 AA; 35479 MW; C761FD6439D27A26 CRC64;
Query Match 92.4%; Score 1498; DB 2; Length 317;
Best Local Similarity 92.4%; Pred. No. 1.4e-104;
Matches 291; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
QY 2 MVDNGNESSATYFLLGLPGLBEAOFMLAPFLCSLVLIANVGLNLTIIYIVRTHSHLP 61
DB 1 MGSBSGNESSVTFILIGLPELSEFQFWLAPFLCSLVLIANVGLNLTIIYIVRTHSHLP 60
QY 62 MYFLCMLSGDILISTSSMPKMLAIFWNSTTIQPDACLQIPAIHSLSGMESTVLLAM 121
DB 61 MYFLCMLSGDILISTSSMPKMLAIFWNSTTIQPDACLQIPAIHSLSGMESTVLLAM 120
QY 122 AFDPRVAICHPRLRATVTLTPRVTKIGVAAVRGAALMAPLPVTKQLPFCRSNIIISHSY 181
DB 121 AFDPRVAICHPRLRATVTLTPRVTKIGVAAVRGAALMAPLPVTKQLPFCRSNIIISHSY 180
QY 182 CLHODVWKLACDDIRVNVYGLIYISALGDSLLISFSYLLILKTIVGLTREAOAKAFG 241
DB 181 CLHODVWKLACDDIRVNVYGLIYISALGDSLLISFSYLLILKTIVGLTREAOAKAFG 240
QY 242 TCVSHVCAVFIFYVPFGLSMVHRPSKRSDPLPVILANITYLVLPVLPNPIVGVKTKEI 301
DB 241 TCVSHVCAVFIFYVPFGLSMVHRPSKRSDPLPVILANITYLVLPVLPNPIVGVKTKEI 300
QY 302 RQRLRLFHVAITMAS 316
DB 301 RQRLRLFLMTHTS 315

RESULT 7
Q6SNE2_9PRIM
ID Q6SNE2_9PRIM PRELIMINARY; PRT; 223 AA.
AC Q6SNE2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
OS Olfactory receptor (Fragment).
DB Olfactoria gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Giald Y., Wiebe V., Przeworski M., Lancel D., Paabo S.;
RT "Loss of Olfactory Receptor Genes Coincides with the Acquisition of
Full Trichromatic Vision in Primates.";
RL PLOS Biol. 2:0120-0125(2004)
DR EMBL; AY454949; AARI9522.1; -; Genom1_c_DNA.

DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
DR Receptor.
FT NON TER 1 1
FT NON TER 223 223
SQ SEQUENCE 223 AA; 24538 MW; E963757D41480412 CRC64;
Query Match 68.6%; Score 1113; DB 2; Length 223;
Best Local Similarity 98.7%; Pred. No. 8.6e-76;
Matches 220; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 67 CMLSGDILISTSSMPKMLAIFWNSTTIQPDACLQIPAIHSLSGMESTVLLAMADRY 126
DB 1 CMLSGDILISTSSMPKMLAIFWNSTTIQPDACLQIPAIHSLSGMESTVLLAMADRY 60
QY 127 VAICHPRLRATVTLTPRVTKIGVAAVRGAALMAPLPVTKQLPFCRSNIIISHSYCLHOD 186
DB 61 VAICHPRLRATVTLTPRVTKIGVAAVRGAALMAPLPVTKQLPFCRSNIIISHSYCLHOD 120
QY 187 WVKLACDDIRVNVYGLIYISALGDSLLISFSYLLILKTIVGLTREAOAKAFGTCVSH 246
DB 121 WVKLACDDIRVNVYGLIYISALGDSLLISFSYLLILKTIVGLTREAOAKAFGTCVSH 180
QY 247 VCAVFIFYVPFGLSMVHRPSKRSDPLPVILANITYLVLPV 289
DB 181 VCAVFIFYVPFGLSMVHRPSKRSDPLPVILANITYLVLPV 223

RESULT 8
Q8BV9_MOUSE
ID Q8BV9_MOUSE PRELIMINARY; PRT; 320 AA.
AC Q8BV9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
OS Olfactory receptor MOR18-2 (Olfactory receptor Olfr78) (Prostate-
specific G protein-coupled receptor RAIc) (Mus musculus 0 day neonate
skin cDNA, RIKEN full-length enriched library, clone:4631413D8
DE product:OLFACTORY RECEPTOR MOR18-2, full insert sequence) (Mus
musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched
library, clone:9630060D12 product:OLFACTORY RECEPTOR MOR18-2, full
insert sequence).
DE Name=Olfr78;
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 5:124-133(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RA Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory
receptor gene families.";
RL Hum. Mol. Genet. 11:535-546(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

[4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykina B.M., Lane R.P., Tomes-Priddy L., Ross J.A.,
Walker M., Williams E.M., Traek B.J.
RT "Odorant receptor expressed sequence tags demonstrate olfactory
RT expression of over 400 genes, extensive alternative splicing and unequal
RT expression levels."
RL Genome Biol. 4:R71-R71(2003).
RN
RN NUCLEOTIDE SEQUENCE.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=BA16/C; PubMed=11707321; DOI=10.1016/S0378-1119(01)00700-0;
RX MEDLINE=21564169; PubMed=11707321; DOI=10.1016/S0378-1119(01)00700-0;
RA Yuan T.T., Toy P., McClary J.A., Lin R.D., Miyamoto N.G.,
RA Kretschmer P.J.
RT "Cloning and genetic characterization of an evolutionarily conserved
RT human olfactory receptor that is differentially expressed across
RT species."
RL Gene 278:41-51(2001).
[7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=2085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi T., Fukuda S.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirini L.M., Strebili F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Offield D., Bojunga M., Carninci P., de Bonaldo M.F.,
RA Grommette M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Nombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Williams L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:665-690(2001).
[9]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi T., Bono H., Kondo S.,
RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yagi K., Tomaru A., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirini L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Karai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurichin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Matsuda L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Piliat R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vercano R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshew-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yamunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
[10]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
[11]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakeguchi S., Ikegami T., Kaishiki M.,
RA Fujiwara S., Inoue K., Togawa Y., Iwata M., Ohara E., Watanabe M.,
RA Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Yoneda Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
[12]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Skin;
RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hirokawa K., Hirokawa T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numata R., Ono M., Ohashi N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yamunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073011; AAL60674.1; -; Genomic DNA.
DR EMBL; AY317674; AAF71053.1; -; Genomic DNA.
DR EMBL; AF378854; AAL35109.1; -; mRNA.
DR EMBL; AK036356; BAC29396.1; -; mRNA.
DR EMBL; AK028467; BAC29366.1; -; mRNA.
DR EMBL; ENSMSG00000043366; Mus musculus.
DR MGI; MGI:2157548; Olf78.
DR GO; GO:0016021; C:Integral to membrane, TAS.
DR InterPro; IPR000276; GPCR_Rhodpn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00245; OLFACTORY.
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE; PS02621; G_PROTEIN_RECIP_F1_2; 1.
DR Receptor.
SQ SEQUENCE 320 AA; 35578 MW; 7161ACABF4328959 CRC64;
Query Match 60.7%; Score 985; DB 2; Length 320;
Best local similarity 59.8%; Pred. No. 5e-66;

Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESSATYVILGLPGLBEAQFMAFLPGLSYLIYAVTGLNLTIIYRTSHSLHEPMYFLC 67
 DB 5 NPTNAT-FVLIGIGLEKQKHFVWGEPPLSMVYVAMFGNCIYVFIYRTSRSLAAPMYFLC 63
 QY 68 MLSGIDILISTSSMPKMLAIFMFNSTTIOFDACLIQIFAIHSLSGESTVLLAAMPDRYV 127
 DB 64 MLAIDILISTSSMPKMLAIFMFNSTTIOFDACLIQIFAIHSLSGESTVLLAAMPDRYV 123
 QY 128 AICPLRHATVLTLPRTVKIGVAAVRGAAALMAPLPVFIKQLPFCRSNLTSHSYCLHODV 187
 DB 124 AICPLRHAAVLTLPRTVKIGVAAVRGAAALMAPLPVFIKQLPFCRSNLTSHSYCLHODV 183
 QY 188 MKLACDDIRVVNVVGLIVTISAIIGDLSLISPSYLLIKTVLGL-TREAOAKAGTCVSH 246
 DB 184 MKLAVADTLPRVNVGLTALILVMGVDMFISLSTYLIIRTVLQPLSKERAKAFCVSH 243
 QY 247 VCAVFIYPVPFISGSMVHRSKRSDPLPVLIANIYLLVPPVLANPIYGVTKRIRORIL 306
 DB 244 IGVTLAFVPLIGLSVHRFGNSLHPVIRVVMGDIYLLPPVINPIYIGAKTKQIRRVL 303
 QY 307 RLPHVA 312
 DB 304 AMFKIS 309

RESULT 10

Q6IF94_HUMAN

Q6IF94_HUMAN PRELIMINARY; PRT; 320 AA.

AC Q6IF94;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DS Olfactory receptor OR11-16.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NC NCB1_Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14983052; DOI=10.1073/pnas.0307882100;
 RA Malnic B., Godfrey P.A., Buck L.B.;
 RT "The human olfactory receptor gene family."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).
 DR EMBL: BK004368; DAA04766.1; -; Genomic DNA.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0004984; F:Olfactory receptor activity; IEA.
 DR GO: GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR InterPro: IPR000725; Olfact_receptor.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PRINTS: PR00245; OLFACTORYR.
 DR PROSITE: PS00237; G_PROTEIN_RECBP_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECBP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 320 AA; 35493 MW; 03582CC2AAB6E2C6 CRC64;

Query Match 60.4%; Score 979; DB 2; Length 320;

Best Local Similarity 59.5%; Pred. No. 1.4e-65;

Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESSATYVILGLPGLBEAQFMAFLPGLSYLIYAVTGLNLTIIYRTSHSLHEPMYFLC 67
 DB 5 NPTNAT-FVLIGIGLEKQKHFVWGEPPLSMVYVAMFGNCIYVFIYRTSRSLAAPMYFLC 63
 QY 68 MLSGIDILISTSSMPKMLAIFMFNSTTIOFDACLIQIFAIHSLSGESTVLLAAMPDRYV 127
 DB 64 MLAIDILISTSSMPKMLAIFMFNSTTIOFDACLIQIFAIHSLSGESTVLLAAMPDRYV 123

QY 128 AICPLRHATVLTLPRTVKIGVAAVRGAAALMAPLPVFIKQLPFCRSNLTSHSYCLHODV 187
 DB 124 AICPLRHAAVLTLPRTVKIGVAAVRGAAALMAPLPVFIKQLPFCRSNLTSHSYCLHODV 183
 QY 188 MKLACDDIRVVNVVGLIVTISAIIGDLSLISPSYLLIKTVLGL-TREAOAKAGTCVSH 246
 DB 184 MKLAVADTLPRVNVGLTALILVMGVDMFISLSTYLIIRTVLQPLSKERAKAFCVSH 243
 QY 247 VCAVFIYPVPFISGSMVHRSKRSDPLPVLIANIYLLVPPVLANPIYGVTKRIRORIL 306
 DB 244 IGVTLAFVPLIGLSVHRFGNSLHPVIRVVMGDIYLLPPVINPIYIGAKTKQIRRVL 303
 QY 307 RLPHVA 312
 DB 304 AMFKIS 309

RESULT 11

O51E2_RAT

O51E2_RAT STANDARD; PRT; 320 AA.

AC O51E2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DS Olfactory receptor 51E2 (G-protein coupled receptor RA1c).
 GN Name=O51e2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 NC NCB1_Taxid=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99131082; PubMed=9932290;
 RA Raming K., Konzelmann S., Breer H.;
 RT "Identification of a novel G-protein coupled receptor expressed in
 distinct brain regions and a defined olfactory zone."
 RL Recept. Channels 6:141-151(1998).
 CC -1- FUNCTION: Putative odorant receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed only in some areas of the brain and
 in the olfactory epithelium.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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 use as long as its content is in no way modified and this statement is not
 removed.

DR EMBL: AF079864; AAD12761.1; -; mRNA.
 DR EMBL: ENSRN00000018606; Rattus norvegicus.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR InterPro: IPR000725; Olfact_receptor.
 DR PANTHER: PTHR11398; Olfact_receptor; 1.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PRINTS: PR00245; OLFACTORYR.
 DR PROSITE: PS00237; G_PROTEIN_RECBP_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECBP_F1_2; 1.
 KM G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
 Receptor; Sensory transduction; Transducer; Transmembrane.
 FT TRANSMEM 1 24
 FT TOPO_DOM 1 45
 FT TRANSMEM 25 45
 FT TOPO_DOM 46 53
 FT TRANSMEM 54 74
 FT TOPO_DOM 75 98
 FT TRANSMEM 99 119
 FT TOPO_DOM 120 138
 FT TRANSMEM 139 159
 FT TOPO_DOM 160 195
 FT TRANSMEM 196 216

FT	TOPO_DOM	217	236	Cytoplasmic (Potential).
FT	TRANSMEM	237	257	6 (Potential).
FT	TOPO_DOM	258	272	Extracellular (Potential).
FT	TRANSMEM	273	293	7 (Potential).
FT	TOPO_DOM	294	320	Cytoplasmic (Potential).
FT	CARBOHYD	5	5	N-linked (GlcNAc...) (Potential).
FT	DISULFID	96	178	By disulfide.
FT	SEQUENCE	320 AA;	35505 MM;	87PF78F5PF5DP94 CRC64;
Query Match		60.2%	Score 977;	DB 1; Length 320;
Best Local Similarity		59.5%	Pred. No. 2e-65;	
Matches	182;	Conservative	53;	Mismatches 69; Indels 2; Gaps 2
QY	:	:	:	:
8	NESSATYFILGLPGLBEAQFWLAEPPLCSLYLIAVAGNLTIIYVIRTEHSLBPMYFLC	67		
5	NFTNAT-PMILIGIPCLBEAHFWGFPGLSMVAVALFGNCIVFVIRTERSLHAPMYLFLC	63		
QY	:	:	:	:
68	MLSGDILISSTSMKPKMLAIPFNSSTIQFDALQIQAHSLSGMSGVLLMAFPDRY	127		
Db	MLAAILDLALSTSTWPKLALFPFDSREIRTFDACLQMFPIHALSAIESITLLAMAFDRY	123		
QY	:	:	:	:
128	AICPPLRAVATLTPTVTIKGVAAVRGAALMAPIPVPIKOLPFGRSNLISHCYADPV	187		
Db	AICPPLRAVATLTPTVTIKGVAAVRGAALMAPIPVPIKOLPFGRSNLISHCYADPV	183		
QY	:	:	:	:
188	MKLACDDIRVAVVYGLIVITISAGLSLLISPSYLLIKTVLGL-TREAQAYAFGCVSH	246		
Db	MKLAVATDLPVNVVYGLTALILVAGVDVWFISLSTYLIRAVLQPLSKSBRAPAFGCVSH	243		
QY	:	:	:	:
247	VCANFIPVVPFPGLSMWRFSGRSRSPVLIANTLYLVPPPLANTIVGVTKERORIL	306		
Db	IGVLAFAVVPFPGLSVHRFGNSLDPIVHVLMDVYLLPVPINPIIGAKTKQIRTEYL	303		
QY	:	:	:	:
307	RLPFHYA	312		
Db	:	:	:	:
304	AMFKIS	309		
RESULT 12				
08VF09 MOUSE				
ID	Q8VF09 MOUSE PRELIMINARY;	PRT;	322 AA.	
AC	Q8VF09;			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-FEB-2005 (TREMBLrel. 29, Last annotation update)			
DE	Olfactory receptor MOR18-3 (Olfactory receptor Olfr557).			
GN	Name=Olfr557;			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=21676863; PubMed=11802173;			
RA	Zhang X., Firestein S.;			
RT	"The olfactory receptor gene superfamily of the mouse."			
RL	Nat. Neurosci. 5:124-133(2002).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;			
RA	Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L.,			
RA	Trask B.J.;			
RT	"Different evolutionary processes shaped the mouse and human olfactory			
RT	receptor gene families."			
RL	Hum. Mol. Genet. 11:535-546(2002).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Adams M.;			
RL	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;			

[illegible]

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RN NUCLEOTIDE SEQUENCE.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsunoto S.,
RA Tetsunmi S., Aburatani H., Asai K., Akiyama Y.:
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RM [2]
RP IDENTIFICATION.
RX PubMed=14983052; DOI=10.1073/pnas.0307882100;
RA Malnic B., Godfrey P.A., Buck L.B.:
RT "The human olfactory receptor gene family."
RL Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).
CC -1- FUNCTION: Putative odorant receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -1- DATABASE: Name=human Olfactory Receptor Data Explorer
(HORDE);
WWW="http://bip.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&value=ORS1D
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB065855; BAC06073.1; -; Genomic DNA.
DR EMBL; BK004370; DA04768.1; -; Genomic DNA.
DR Ensembl; ENSG00000197428; Homo sapiens.
DR HGNC; HGNC:15193; ORS1D.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR00245; OLFACTORTX.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECPE_F1_2; 1.
KM G-protein coupled receptor; Multigene family; Olfaction; Receptor;
KM Sensory transduction; Transducer; Transmembrane.
FT TOPO_DOM 1 38 Extracellular (Potential).
FT TRANSMEM 39 59 1 (Potential).
FT TOPO_DOM 60 67 Cytoplasmic (Potential).
FT TRANSMEM 68 88 2 (Potential).
FT TOPO_DOM 89 112 Extracellular (Potential).
FT TRANSMEM 113 133 3 (Potential).
FT TOPO_DOM 134 152 Cytoplasmic (Potential).
FT TRANSMEM 153 173 4 (Potential).
FT TOPO_DOM 174 209 Extracellular (Potential).
FT TRANSMEM 210 230 5 (Potential).
FT TOPO_DOM 231 250 Cytoplasmic (Potential).
FT TRANSMEM 251 271 6 (Potential).
FT TOPO_DOM 272 285 Extracellular (Potential).
FT TRANSMEM 286 306 7 (Potential).
FT TOPO_DOM 307 324 Cytoplasmic (Potential).
FT DISULFID 110 202 By similarity.
SQ SEQUENCE 324 AA; 35839 MW; 52401F88565E3BD1 CRC64;

Query March 57.8%; Score 937.5; DB 1; Length 324;
Blast Local Similarity 58.5%; Pred. No. 1.9e-62;
Matches 179; Conservative 52; Mismatches 72; Indels 3; Gaps 3;
6 NGSSSATYFLILGLPGI-EEAQEWLAPPLCSLYLIALVGNLTIIVYRTSHSLPEPYI 64
15 NGNLVHAAYFLVNGVPGIPIHFLAPPLCFMYALATLGNLTIIVLIRVERRLHEPYL 74
65 FLCMLSGIDILITSSMPKMLAIFWNSTTQPDACLIQITAIHSLSGMESTVLIAMAFD 124
75 FLAMLTSTDLVSSITMPKMSLFLMGIQIEIFNICLQWELIHALSAVESAVLIAMAFD 134
125 RYVAICHLRAATVLTPLRVTKIGVAAVVGAALMAPIPVITKOLPFCRSNIIHSGVGLH 184
135 RFAICHLRAHSAVLTGCTVAKIGLSALTGRGVFPPLPITLKMISYCQTHVTHSPCLH 194
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QY 185 QDVAKLACDDIRVVVYGLIIVISAIGLDLSISFYLLILKTVLGH-TREAQKAEGTC 243
DB 195 QDINKSCSTIRVVVYGLPIILISVMGVDSLFIGFSIILIMANVLEBSRAALAKANTC 254
QY 244 VSHVCAVFITYVFPPIGLSMVHRFSKRSDPLPVILANIYLLVPPVLPNIYGVTKKIRQ 303
DB 255 ISHLCAVLVFPVPLIGLSVVRILG-GPTSLHVMANTYLLPVPVPLVYGAKTKKICS 313
QY 304 RIILPLF 309
DB 314 RVLQMF 319

RESULT 14
Q8VH05_MOUSE PRELIMINARY; PRT; 315 AA.
ID Q8VH05_MOUSE
AC Q8VH05
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE Olfactory receptor MOR10-1 (Olfactory receptor Olfr555).
GN Name=Olfr555;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.:
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 5:124-133(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RA Trask B.J.:
RT "Different evolutionary processes shaped the mouse and human olfactory
RT receptor gene families."
RL Hum. Mol. Genet. 11:535-546(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.:
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Trask B.J.:
RT "Odorant receptor expressed sequence tags demonstrate olfactory
RT expression of over 400 genes, extensive alternate splicing and unequal
RT expression levels."
RL Genome Biol. 4:R71-R71(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Sanders K.:
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072983; AA060646.1; -; Genomic DNA.
DR EMBL; AY317668; AAP1047.1; -; Genomic DNA.
DR Ensembl; ENSMUSG00000049196; Mus musculus.
DR MGI; MGI:3030389; Olfr555.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; C:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
```


DR	PRINTS: PR00245; OLFACTOROR.
DR	PROSITE, PS00237; G_PROTEIN_RECPE_P1.1; UNKNOWN_1.
DR	PROSITE, PS50262; G_PROTEIN_RECPE_P1.2; 1.
RW	Receptor.
SQ	SEQUENCE 315 AA; 35157 MW; BAA50BF966E3F0A9 CRC64;
	Query Match 56.4%; Score 914.5; DB 2; Length 315;
	Best Local Similarity 54.5%; Pred. No. 9,7e-61;
	Matches 168; Conservative 65; Mismatches 74; Indels 1; Gaps 14;
QY	3 VDPNGNSASATYFPIIGHGLGEAEAFMLAPPLCSYLLAVLGNTLIYIVRTREHSLHSPM 62
DB	1 MNSASQCNHNSFILITGIPGPHDKPKPMAPFGPIYITLGLNGITLAVVYEGSLHSPM 60
QY	63 YIFCLMISGIDILISTSSMPKMLAFWNSFTTIOFACLQIFAIHSLSGNESTVLLAMA 122
DB	61 YFPICLIALTIVSLISMSTLPSMLSTIFWNADEIPDADICIQPFHIGRGVSEGLVEMA 120
QY	123 PDRYVALHPRLHATVLTLPKVTIKGVAAVVRGALAMPVPVFIKQLPFGCSNIIISHYC 182
DB	121 PDRFVALRDPRLRYASILTHGILGKIGLVLLAAVACVVPVDFLIRLPFCRSNVLISHYC 180
QY	183 LHODPMKACCDIRNVVYGLIVITSAIGDLSLISPSYLLIKTVLGL-TREAQAKAFG 241
DB	181 LHQDMRLACASTRNSLSYGLVLLITGLDMLITLFSYVLTKVLSIGSAEERKLKLN 240
QY	242 TCVSHVCAVPIFYVPPIGLSMVHVRPSKRDSEPLPILANITYLLVPPVLPVYGVKTEI 301
DB	241 TCLSHIGAVLLPYIFLIGATVTHRRGKRLSPVHMFMANITYLLPVPVLPVYSVKTKQI 300
QY	302 KQRIIRLF 309
DB	301 RRRRIIOVF 308
RESULT 15	
Q8VH11_MOUSE	
AC	Q8VH11_MOUSE PRELIMINARY; PRT; 312 AA.
DT	01-MAR-2002 (TREMBLrel. 20, Created)
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT	01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE	Olfactory receptor MOR-2 (Olfactory receptor Olfr577).
GN	Name=Olfr577;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RN	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=21676863; PubMed=11802173;
RA	Zhang X., Piretschik S.,
RT	"The olfactory receptor gene superfamily of the mouse."
RL	Nat. Neurosci. 5:124-133(2002).
RN	[2]
RN	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RA	Young J.M., Friedman C., Williams E.M., Rose J.A., Tomner-Priddy L.,
RT	Trask B.J.;
RT	"Different evolutionary processes shaped the mouse and human olfactory
RL	receptor gene families."
RN	Hum. Mol. Genet. 11:535-546(2002).
RN	[3]
RN	NUCLEOTIDE SEQUENCE.
RA	Adams M.;
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN	[4]
RN	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA	Young J.M., Shykind B.M., Lane R.P., Tomner-Priddy L., Rose J.A.,
RA	Walker M., Williams E.M., Trask B.J.;
RT	"Odorant receptor expressed sequence tags demonstrate olfactory

RT	expression of over 400 genes, extensive alternate splicing and unequal
RL	expression levels.",
RL	Genome Biol. 4:R71-R71(2003).
RN	[5]
RP	NUCLEOTIDE SEQUENCE.
RA	Sanders K.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY072977; AA60640.1; -, Genomic DNA.
DR	EMBL; AY171692; AAP1065.1; -, Genomic DNA.
DR	Ensembl; ENSMUSG0000043354; Mus musculus.
DR	MGI; MGI:3030411; Olfcr577.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0004984; F:olfactory receptor activity; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR	GO; GO:0007165; P:signal transduction; IEA.
DR	InterPro; IPR000276; GPCR_Rhodop.
DR	InterPro; IPR000725; Olfact_receptor.
DR	PANTHER; PTHR11398; Olfact_receptor; 1.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRHOPOSN.
DR	PRINTS; PR00245; OLFACTORYR.
DR	PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; UNKNOWN_1.
DR	PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
KW	Receptor.
SQ	SEQUENCE 312 AA; 34575 MW; CD233B37732052B5 CRC64;
Query Match	55.6%; Score 901.5; DB 2; Length 312;
Best Local Similarity	53.2%; Pred. No. 9,2e-60;
Matches 165; Conservative 63; Mismatches 81; Indels 1; Gaps 1;	
Qy	1 MMDVDPNGNESSATYFIIIGLPGIEEAQFWLAPFLCSLYLAVGNLTITTYIVRTESLHE 60
Db	1 MTPPEPLGNGSSSTFPLSGIPGHEHMIWISLPLCLMYIVSLIGNCITLLFIKTEPSLHE 60
Qy	61 PMYIFLCMLSSIDLITSSMFKRLAFWNRSTTIQPDACLLQFPAHSHSGMESTVILA 120
Db	61 PMYIFLNLMLATDGLSLCTPLFVLGIFWVGARDISHDACPTQLFPHCHSFLSSVLLS 120
Qy	121 MAPPRYVALCHPLRHATVTLTPRVTKIGVAAVVGAALMAPLPFIRKQLPFCRSNIISHS 180
Db	121 MAPPRFPAICRPLHAYASILTHVTVYRIGLMSLGSAVALIFPLPMLAKRPFCGLSVLSHS 180
Qy	181 YCLHQDVWKLACDDIRVVNVYGLIVISAIGLDSLLISFSYLLILKTVLGL-TREAQAKA 239
Db	181 YCLHQEWKLCACADIKANSIYGMFVIVSTVGVDLILFSAVALIRVTLGIASPAERLKA 240
Qy	240 FGTGVSHVCAVFIYVYVFIIGLSMWRHSKRRDSELPYITANITYLVVPPVNLPIYGYKTK 299
Db	241 LMTGVSHISAVLTETTEMIGLSVTHRGKQAPHLVQVWGVVLLFPVWNPPIYVSXTK 300
Qy	300 EIRORILRLP 309
Db	301 QIRDRVAHAF 310
RESULT 16	
OSIG2 HUMAN	
ID OSIG2_HUMAN	STANDARD; PRT; 314 AA.
AC Q8NGK0;	
DT 10-OCT-2003 (Rel. 42, Created)	
DT 10-OCT-2003 (Rel. 42, Last sequence update)	
DT 13-SEP-2005 (Rel. 48, Last annotation update)	
DE Olfactory receptor 51G2.	
OS Name=OR51G2;	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;	
OC Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RA Suwa M., Sato T., Okouchi I., Arita M., Futani K., Matsumoto S.,	

```

Ra Tautumi , Aburatani H., Asai K., Akiyama Y.;
Rt "Genome-wide discovery and analysis of human seven transmembrane helix
RL receptor genes.";
CC Submitted (JUL-2001) to the EMBL/genbank/DBSJ databases.
CC -I FUNCTION: Putative odorant receptor.
CC -I SUBCELLULAR LOCATION: Integral membrane protein.
CC -I SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -I DATABASE: NAME=human Olfactory Receptor Data Explorer|unim
(CORDE);
WWW="http://dbip.welzmann.ac.il/cgi-bin/CORDE/showGene.pl?key=symbol&val=ORS161";
-----
Cc This Swiss-Pro entry is copyright. It is produced through a collaboration
Cc between the Swiss Institute of Bioinformatics and the EMBL outstation -
Cc the European Bioinformatics Institute. There are no restrictions on its
Cc use as long as its content is in no way modified and this statement is not
Cc removed.
-----
Cc EMBL; AB065794; BAC06013.1; -; Genomic DNA.
DR Ensembl; ENSG00000176893; Homo sapiens.
DR HGNC; HGNC:15198; ORS162.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7cm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.
KM G-protein coupled receptor; Glycoprotein; Multigene family; Olfaction;
KW Receptor; Sensory transduction; Transducer; Transmembrane.
FT TOPO_DOM 1 30 Extracellular (Potential).
FT TRANSMEM 31 51 Cytoplasmic (Potential).
FT TOPO_DOM 52 59 Extracellular (Potential).
FT TRANSMEM 60 80 Extracellular (Potential).
FT TOPO_DOM 81 104 Extracellular (Potential).
FT TRANSMEM 105 125 Cytoplasmic (Potential).
FT TOPO_DOM 126 144 Extracellular (Potential).
FT TRANSMEM 145 165 Extracellular (Potential).
FT TOPO_DOM 166 201 Extracellular (Potential).
FT TRANSMEM 202 222 Cytoplasmic (Potential).
FT TOPO_DOM 223 242 Extracellular (Potential).
FT TRANSMEM 243 263 Extracellular (Potential).
FT TOPO_DOM 264 278 Extracellular (Potential).
FT TRANSMEM 279 299 Cytoplasmic (Potential).
FT TOPO_DOM 300 314 N-linked (GlcNAc..)(Potential).
FT CARBOHYD 8 8 By similarity.
FT DISULFID 102 194
SQ SEQUENCE 314 AA; 35012 MW; 97DD37BE1F3B9576C CRC64;

Query Match      55.0%; Score 892.5; DB 1; Length 314;
Beat Local Similarity 52.5%; Pred. No. 4,4e-59;
Matches 160; Conservative 63; Mismatches 81; Indels 1; Gaps 1;

6 NGNESSATYFILIGPGLEBAQFMFLAPPLCYSLYLAVNGNTLIIVRTSHSEHPWIF 65
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
8 NSSSSVSAITFLISGLFGELERMAHIWISTIPLCFYLVTSIEGCITLLTIITKRSIHPPMILF 67

Db LCMLSGDILISTSSMPKMLAFWNFSSTTIOFDACLIOFAIHSLSGMSVTYLLAMAEDR 125
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
68 LSMALTDIGLSLTLPYVLGIFFWGARRISHDACPAQLFHCPSPLESSVTLSMARDR 127

Oy VVALTHPRLRHATVLTLPRTKTGVAAVVRGAALLMAPLRPIFIQQLPFCCSNIIISHYCIIHQ 185
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db FVAICHPLAHYSITLNTVIIGRIGLVSIGSVAILPEPLPKMRFPYCGSPVLSHSYCLIQ 187

Oy 126 VVALTHPRLRHATVLTLPRTKTGVAAVVRGAALLMAPLRPIFIQQLPFCCSNIIISHYCIIHQ 185
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 128 FVAICHPLAHYSITLNTVIIGRIGLVSIGSVAILPEPLPKMRFPYCGSPVLSHSYCLIQ 187

Oy 186 DVMKLACADDIRVVNVVYGILVISAIGDSILSFSYLLIKTKVLGLITREBAQA-KAEGTCV 244
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 188 EVMKLACADMKNKSNIYGMVFVISYTGIDSLILTFEYALIRKTVLISAAREFKALANCV 247

Oy 245 SHVCADVLFPTVPDFIGLSMVHRFSKRDSPLPYITALNIYLVLPVLANPIYGYVKYEIKQR 304
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 248 SHICAVLLFETPMIGLIVSIHRFGKAAPHLVQVWMGFMYILLFPVNMMPIVSYKXQIIDR 307

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QY	305	ILRLP	309
DB	308	VTNAP	312
RESULT 17			
ID	061FH7	HUMAN	
AC	061FH7		
DT	05-JUN-2004	(Tremblrel_27, Created)	
DT	05-JUN-2004	(Tremblrel_27, Last sequence update)	
DT	05-JUN-2004	(Tremblrel_27, Last annotation update)	
DS	Olfactory receptor OR11-28.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	PubMed=14983052; DOI=10.1073/pnas.0307882100;		
RA	Malnic B., Godfrey P.A., Buck L.B.;		
RT	"The human olfactory receptor gene family";		
RL	Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).		
DR	EMBL; BK004285; DA004683.1; -; Genbank; DNA.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0004984; F:olfactory receptor activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.		
DR	InterPro; IPR000276; GPCR_Rhodopn.		
DR	InterPro; IPR00725; Olfact_receptor.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCR_RHODOPN.		
DR	PRINTS; PR00245; OLFACTORYR.		
DR	PROSITE; PS00237; G PROTEIN RCCEP F1.1; UNKNOWN_1.		
DR	PROSITE; PS50262; G_PROTEIN_RCBCEP_F1_2; 1.		
KW	Receptor.		
SQ	SEQUENCE 314 AA; 35012 MW; 97D037E1F38E976C CRC64;		
Query Match 55.0%; Score 892.5; DB 2; Length 314;			
Best Local Similarity 52.5%; Pred. No. 4.4e-59;			
Matches 160; Conservative 63; Mismatches 81; Indels 1; Gaps 1;			
QY	6	NGNESSATYPLICPGLEEAQFLAPLCSLYLIANVLGNITYYIRTERSHRPYIF	65
DB	8	NSSSSVATPLSGIPGLERHWIWSIPLCFMYLVSIPGCTLIIFIKTERSHRPYIF	67
QY	66	LCMLSGDIIISTSMRPMKLAIFWENSTIOFDACLQIPAIHSLSGMESTVLAMAFDR	125
DB	68	LSMLALIDGLSLCTLPVTVGIFWVGAREISHDCRQQLPIIHCRPSLESSVLSMAFDR	127
QY	126	VVALCHPLRHATVTLTPRVTKIGVAAVVRCAGALMAPLPVFIKQLPFCRSNITLSYCLHQ	185
DB	128	FVALCHPLRHATVTLTPRVTKIGVAVGRSVALLPPLPFLMKRPYCGSPVLSHSYCLHQ	187
QY	186	DWMLGADDIRVNVVGLIVISAIAGDSLISSYLLIKTVLGLTRDAQ-KAFGCV	244
DB	188	EVMGLADGDMKANSIYGMFVIVSVGIDSLILFYSVALIKTVLSTIASRARRPANTCV	247
QY	245	SHVCAVEIFVYVPGISLMVRHSRRDPSPLPILANITYLLVPVLPNPIVVGVTKEIROR	304
DB	248	SHICAVALLFTPMGLGVIRHFGQAGHVLVGVNMGFVYLLFPVMMPIVVSVKTKQLRDR	307
QY	305	ILRLP	309
DB	308	VTNAP	312
RESULT 18			
ID	08VH17	MOUSE	
AC	08VH17		
DT	01-MAR-2002	(Tremblrel_20, Created)	
DT	01-MAR-2002	(Tremblrel_20, Created)	
DT	01-MAR-2002	(Tremblrel_20, Created)	
DS	Olfactory receptor OR11-28.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	PubMed=14983052; DOI=10.1073/pnas.0307882100;		
RA	Malnic B., Godfrey P.A., Buck L.B.;		
RT	"The human olfactory receptor gene family";		
RL	Proc. Natl. Acad. Sci. U.S.A. 101:2584-2589(2004).		
DR	EMBL; BK004285; DA004683.1; -; Genbank; DNA.		
DR	GO; GO:0016021; C:integral to membrane; IEA.		
DR	GO; GO:0004984; F:olfactory receptor activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.		
DR	InterPro; IPR000276; GPCR_Rhodopn.		
DR	InterPro; IPR00725; Olfact_receptor.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCR_RHODOPN.		
DR	PRINTS; PR00245; OLFACTORYR.		
DR	PROSITE; PS00237; G PROTEIN RCCEP F1.1; UNKNOWN_1.		
DR	PROSITE; PS50262; G_PROTEIN_RCBCEP_F1_2; 1.		
KW	Receptor.		
SQ	SEQUENCE 314 AA; 35012 MW; 97D037E1F38E976C CRC64;		
Query Match 55.0%; Score 892.5; DB 2; Length 314;			
Best Local Similarity 52.5%; Pred. No. 4.4e-59;			
Matches 160; Conservative 63; Mismatches 81; Indels 1; Gaps 1;			

DT 01-MAR--2002 (TREMBLrel. 20, last sequence update)
DT 01-FEB--2005 (TREMBLrel. 29, last annotation update)
DE Olfactory receptor MOR-7.1 (Olfactory receptor Olfr578) .
GN Name=Olfr578;
GN Mus musculus (Mouse) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The Olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 5:124-133(2002) .
RN [2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=21864968; PubMed=11875048; DOI=10.1093/nmg/11.5.535;
RA Young J.M., Friedman C., Williams E.M., Rose J.A., Tomes-Priddy L.,
RA Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory
RT receptor gene families.";
RL Hum. Mol. Genet. 11:535-546(2002) .
RN [3]
RN NUCLEOTIDE SEQUENCE.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22874002; PubMed=14611557; DOI=10.1186/db-2003-4-11-r71;
RA Young J.M., Snykand B.M., Lane R.P., Tomes-Priddy L., Rose J.A.,
RA Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory
RT expression of over 400 genes, extensive alternate splicing and unequal
RT expression levels.";
RL Genome Biol. 4:R71-R71(2003) .
RN [5]
RN NUCLEOTIDE SEQUENCE.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072971; AAL60634.1; -, Genomic DNA.
DR EMBL; AY317693; AAP71066.1; -, Genomic DNA.
DR Ensembl; ENSMUSG00000045792; Mus musculus .
DR MGI; MGI:3030412; Olfr578.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; P:olfactory receptor activity; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007186; P:g-protein coupled receptor protein signaln. . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor .
DR PANTHER; PTHR11398; Olfact_Receptor; 1.
DR Pfam; PF00001; 7tm1.1 .
DR PRINTS; PR00237; GPCRHDOPSN.
DR PROSITE; PRO0245; OLFACTORXR.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
KW Receptor .
SQ SEQUENCE 313 AA, 35682 MW, 39476BD3FPD201D6C CRC64;

Query Match 54.1%; Score 877; DB 2; Length 313;
Best Local Similarity 51.8%; Pred. No. 6, 4e-58;
Matches 158; Conservative 72; Mismatches 73; Indels 2; Gaps 2

QY 6 NGNESATYFLLIGLGLGEADQFWLAFPLCSLYLIVAVLGNLTIIYIVRTSHSLHEPMYIF 65
DB 6 NSSLSQKATVF-LTGQGLSEFHWGWSIPSCSYLIVLGNLTIIIVIRDATLHEPMYIF 64

QY 66 LCMISGIDILISTSGSPKMLAIFWFSNTSTIQFDACLLQIFAISLGMSESTVLAAAFDR 125
DB 65 LAMALALTDGLGLSTLPTVYLGIFWFPARKEIGIPACTQGLFFHTLSLVSSSVLMSGFSR 124
QY 126 YVAICHPILRHATVLTLPVVTYKIGVAAVVEGAAVLAAPLVFPIKQLPFCRSNLTSHSYCLHQ 185

Db	125	YVALCNPLRYSTLTLPRLIVKNGSSVRSALLIPLPFLTKRHYCHSHVLAHYCLHL	184
QY	186	DVKLACDDIRVNVVGVGLIVIIISAIGLSDLIISFSYLLIKTVLG-LTREAKAFGTCV	244
Db	185	EIMKACSSIIYNHVIYGLFVACTGVGVDLLIFLSTYLLIILAVGKASRGRRLALMTCI	244
QY	245	SHVCAVFIFYVPPFGLSMWHRFSKRSDPLPVILLANIYLVPPVPLNPIYGVKTKEIROR	304
Db	245	SHICATLRYIPIWIGLSTVHRGEBH.PRIVHLMSYVYLVPPLNPIVYSIKTKQIROR	304
QY	305	ILRLP 309	
Db	305	ILRKF 309	
RESULT 19			
OBVG26_MOUSE			
ID	OBVG26_MOUSE	PRELIMINARY;	PRT; 314 AA.
AC	OBVG26;		
DT	01-MAR-2002 (Tremblrel, 20, Created)		
DT	01-MAR-2002 (Tremblrel, 20, Last sequence update)		
DT	01-FEB-2005 (Tremblrel, 29, Last annotation update)		
DE	Olfactory receptor MOR14-2 (Olfactory receptor Olftr561).		
GN	Name=Olftr561;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NCBLOTIDE SEQUENCE.		
RX	MEDLINE=21676863; PubMed=11802173;		
RA	Zhang X., Firestein S.;		
RT	"The olfactory receptor gene superfamily of the mouse."		
RL	Nat. Neurosci. 5:124-133(2002).		
RN	[2]		
RP	NCBLOTIDE SEQUENCE.		
RX	MEDLINE=11864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;		
RA	Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priiddy L.,		
RA	Trask B.J.;		
RT	"Different evolutionary processes shaped the mouse and human olfactory		
RT	receptor gene families."		
RL	Hum. Mol. Genet. 11:535-546(2002).		
RN	[3]		
RP	NCBLOTIDE SEQUENCE.		
RA	Adams M.;		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	NCBLOTIDE SEQUENCE.		
RX	MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;		
RA	Young J.M., Shykind B.M., Lane R.P., Tonnes-Priiddy L., Ross J.A.,		
RA	Walker M., Williams E.M., Trask B.J.;		
RT	"Odorant receptor expressed sequence tags demonstrate olfactory		
RT	expression of over 400 genes, extensive alternate splicing and unequal		
RT	expression levels."		
RL	Genome Biol. 4:R71-R71(2003).		
RN	[5]		
RP	NCBLOTIDE SEQUENCE.		
RA	Sanders K.;		
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY072994; AAL60657.1; -; Genomic DNA.		
DR	EMBL; AY317676; AAP71055.1; -; Genomic DNA.		
DR	Ensembl; ENSMUSG0000051711; Mus musculus.		
DR	MGI; MGI:3030395; Olftr561.		
DR	GO; GO:0016021; C:Integral to membrane, IEA.		
DR	GO; GO:0004984; F:Olfactory receptor activity, IEA.		
DR	GO; GO:0004872; F:receptor activity, IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signaln. .; IEA.		
DR	GO; GO:0007165; P:signal transduction, IEA.		
DR	InterPro; IPR000276; GPCR_Rhodopsn.		
DR	InterPro; IPR00725; Olfact_receptor.		
DR	PANTHER; PTHR11398; Olfact_receptor.1.		

DR Pfam; PF00001; 7cm 1; 1.
 DR PRINTS; PR00237; GPCRHOOPRN.
 DR PROSITE; PR00245; OLFACTORYR.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
 KW Receptor.
 SQ SEQUENCE 314 AA; 35096 MW; 9F1016F8B1A040B9 CRC64;
 Query Match 54.0%; Score 875.5; DB 2; Length 314;
 Best Local Similarity 52.3%; Pred. No. 8.3e-58;
 Matches 162; Conservative 63; Mismatches 82; Indels 3; Gaps 2;
 QY 5 PNGESSA--TYFLIGLPGLEBAQFMAFLPCLSLYLIVAGNLTIIVYRTEHSLHEP 62
 2 PSFNESTAYPVFVLTGIPGLESHWTMISIFPCCLVIAISGNMILFVITTESSLHEP 61
 QY 63 YIFLCMLSGDILISTSSMPKMLAIFWNSITTIQPDACLIQIPAHISLGMESTVLLMA 122
 62 YIFLSMLSTFDLIGLSTLVVLGIFWFMVBIISFDACIGMFIHGFTESSVLLVMA 121
 QY 123 FDRVVAICHLRHAATVLTLPRTKIGVAAVVRAALMAFLPVFIKOLPFCRSNLSHSYC 182
 122 FDRFALCNPRKRMILNRSKIIIVGFAITIRGTTALVPLLLKRLSFCRSVLAHSYC 181
 QY 183 LHODVWLACDDIRVNVVGLIVITSAIGLDSLISFSYLLIKTYLGL--TRBAQAKAF 241
 182 FHPDVWLKSGDTRINSAGLAIIVSTAGLDSVLILSLVYLIIHSVLCIASKEBKAKAF 241
 QY 242 TCVSHVCAVPIFYVPIGLSMVHRFSKRDSPLVILANTILVLPPLNPIVGVTKKEI 301
 242 TCVSHLAAVAILFYIPMISLSLHFRFGKAPPVHTLIANVLLIPVWNPPIYSVKTKQI 301
 QY 302 RQRIIRLEPHV 311
 302 RKAMLKVPV 311
 Db 302 RKAMLKVPV 311
 Db 302 RKAMLKVPV 311
 RESULT 20
 Q8VG22 MOUSE
 ID Q8VG22_MOUSE PRELIMINARY; PRT; 314 AA.
 AC Q8VG22;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
 DE Olfactory receptor MOR30-1 (Olfactory receptor Olfr569).
 GN Name=Olfr569;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21676863; PubMed=11802173;
 RA Zhang X., Firestein S.;
 RT "The Olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 5:124-133(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
 RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
 RA Trask B.U.;
 RT "Different evolutionary processes shaped the mouse and human olfactory
 RT receptor gene families";
 RL Hum. Mol. Genet. 11:535-546(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,

RA Walker M., Williams E.M., Trask B.U.;
 RT "Olfactory receptor expressed sequence tags demonstrate olfactory
 RT expression of over 400 genes, extensive alternative splicing and unequal
 RT expression levels";
 RL Genome Biol. 4:R71-R71(2003).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RX EMBL; AY072998; AL60661.1; -; Genomic DNA.
 DR EMBL; AY17684; AAP71059.1; -; Genomic DNA.
 DR EMBL; ENSMUSG0000062142; Mus musculus.
 DR MGI; MGI:3030403; Olfr569.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004984; F:olfactory receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR000725; Olfact_receptor.
 DR PANTHER; PTHR11398; Olfact_receptor; 1.
 DR Pfam; PF00001; 7cm 1; 1.
 DR PRINTS; PR00237; GPCRHOOPRN.
 DR PRINTS; PR00245; OLFACTORYR.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.
 KW Receptor.
 SQ SEQUENCE 314 AA; 35578 MW; 718BFB2F351F669 CRC64;
 Query Match 53.9%; Score 873.5; DB 2; Length 314;
 Best Local Similarity 50.2%; Pred. No. 1.2e-57;
 Matches 155; Conservative 68; Mismatches 85; Indels 1; Gaps 1;
 QY 2 MDPNGESSATYFPIIGLPGLEBAQFMAFLPCLSLYLIVAGNLTIIVYRTEHSLHEP 61
 1 MVASNSNSSHPILFFMLGIGLENYQFMAFPFCWATIVLTGNTITLYIRIDHTLHEP 60
 QY 62 MYFLCMLSGDILISTSSMPKMLAIFWNSITTIQPDACLIQIPAHISLGMESTVLLAM 121
 61 MYFLALATLTDVLSSSTQPKMALILMFHSHEIRVNACLIQVFIHAFSBSGVLMTM 120
 QY 122 AFDRYVVAICHLRHAATVLTLPRTKIGVAAVVRAALMAFLPVFIKOLPFCRSNLSHSY 181
 121 ALDRYVVAICPLRHSSTLITTSVYIKGAAVVAGLWVSPFCFVMSMPCKPKVLPQSY 180
 QY 182 CLHODVWLACDDIRVNVVGLIVITSAIGLDSLISFSYLLIKTYLGL--TRBAQAKAF 240
 181 CEMAVLKLCACTRYVNRGIGLVAFSVGFDIIVISVSVMLBRAVLRLPSEGAUKAF 240
 QY 241 GTCVSHVCAVPIFYVPIGLSMVHRFSKRDSPLVILANTILVLPPLNPIVGVTKKE 300
 241 GTCASHVCVILAFYIPALPFLTLRFGHNVRVYVIMFANFYLLVPMNLPIYGVATKQ 300
 QY 301 IRQRIIRLEP 309
 301 IRDRIKRGF 309
 Db 301 IRDRIKRGF 309

Search completed: March 9, 2006, 08:29:14
 Job time : 234 secs

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OM protein - protein search, using sw model

Run on: March 9, 2006, 08:29:29 ; Search time 46 Seconds
(without alignments)
571.541 Million cell updates/sec

Title: US-10-001-469A-2866
Perfect score: 1622
Sequence: 1 MWVDPNGSSATRYFLIGL.....KEIRQRILNLFVHTASRP 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCTRUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/R_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1619	99.8	318	2	US-09-759-143-920
2	1619	99.8	318	2	US-10-012-896-920
3	1617	99.7	317	2	US-09-680-728-2
4	1617	99.7	317	2	US-10-017-066A-2
5	979	60.4	320	2	US-09-439-313-527
6	979	60.4	320	2	US-09-636-215-527
7	979	60.4	320	2	US-09-685-166A-527
8	979	60.4	320	2	US-09-679-426-527
9	979	60.4	320	2	US-09-759-143-527
10	979	60.4	320	2	US-09-651-236-527
11	979	60.4	320	2	US-09-668-033C-4
12	979	60.4	320	2	US-09-657-279-527
13	979	60.4	320	2	US-10-012-896-527
14	977	60.2	320	2	US-09-680-728-3
15	977	60.2	320	2	US-10-017-066A-3
16	965.5	59.5	320	2	US-09-968-033C-2
17	964.5	59.5	320	1	US-08-465-980-2
18	964.5	59.5	320	1	US-09-053-303-2
19	964.5	59.5	320	2	US-09-339-115-2
20	964.5	59.5	320	2	US-09-680-728-4
21	964.5	59.5	320	2	US-10-017-066A-4
22	964.5	59.5	320	4	PCT-US95-07093-2
23	427.5	26.4	314	2	US-08-968-876-7
24	427.5	26.4	314	2	US-09-968-033C-5
25	413.5	25.5	340	2	US-09-546-986A-6
26	413.5	25.5	340	2	US-09-524-730-6
27	402.5	24.8	310	2	US-09-546-986A-2

28	402.5	24.8	310	2	US-09-524-730-2	Sequence 2, Appli
29	394.5	24.3	309	2	US-08-988-876-5	Sequence 5, Appli
30	387.5	23.9	334	2	US-09-546-986A-8	Sequence 8, Appli
31	387.5	23.9	334	2	US-09-524-730-8	Sequence 8, Appli
32	383	23.6	333	2	US-08-988-876-6	Sequence 6, Appli
33	374	23.1	313	2	US-09-465-901-48	Sequence 4, Appli
34	367	22.6	296	2	US-08-467-948A-2	Sequence 2, Appli
35	367	22.6	296	2	US-08-467-947A-2	Sequence 2, Appli
36	358.5	22.1	327	2	US-08-748-506-24	Sequence 24, Appli
37	357.5	22.0	247	1	US-08-465-980-3	Sequence 3, Appli
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39	357.5	22.0	247	4	US-09-339-115-3	Sequence 3, Appli
40	357.5	22.0	247	4	PCT-US95-07093-3	Sequence 3, Appli
41	357.5	22.0	316	1	US-08-827-291A-2	Sequence 2, Appli
42	355.5	21.9	284	4	US-08-118-270-61	Sequence 61, Appli
43	355.5	21.9	284	4	PCT-US93-08528-61	Sequence 61, Appli
44	354.5	21.9	331	2	US-08-748-506-20	Sequence 20, Appli
45	351.5	21.7	321	2	US-08-748-506-12	Sequence 12, Appli
46	348	21.5	331	2	US-08-748-506-18	Sequence 18, Appli
47	347	21.4	284	1	US-08-118-270-67	Sequence 67, Appli
48	347	21.4	284	4	PCT-US93-08528-67	Sequence 67, Appli
49	345.5	21.3	321	2	US-08-748-506-13	Sequence 13, Appli
50	345	21.3	321	2	US-08-748-506-10	Sequence 10, Appli
51	339.5	20.9	293	1	US-08-118-270-60	Sequence 60, Appli
52	339.5	20.9	293	4	PCT-US93-08528-60	Sequence 60, Appli
53	337.5	20.8	327	2	US-08-748-506-14	Sequence 14, Appli
54	335.5	20.7	277	1	US-08-118-270-62	Sequence 62, Appli
55	335.5	20.7	277	4	PCT-US93-08528-62	Sequence 62, Appli
56	332.5	20.5	327	2	US-08-748-506-22	Sequence 22, Appli
57	332.5	20.5	327	2	US-08-748-506-23	Sequence 23, Appli
58	329	20.3	277	4	US-08-118-270-68	Sequence 68, Appli
59	329	20.3	277	4	PCT-US93-08528-68	Sequence 68, Appli
60	329	20.3	321	2	US-08-748-506-11	Sequence 11, Appli
61	326	20.1	286	1	US-08-118-270-65	Sequence 65, Appli
62	326	20.1	286	4	PCT-US93-08528-65	Sequence 65, Appli
63	326	20.1	331	2	US-08-748-506-19	Sequence 19, Appli
64	320	19.7	273	1	US-08-118-270-63	Sequence 63, Appli
65	320	19.7	273	4	PCT-US93-08528-63	Sequence 63, Appli
66	320	19.7	274	1	US-08-118-270-69	Sequence 69, Appli
67	320	19.7	274	4	PCT-US93-08528-69	Sequence 69, Appli
68	318.5	19.6	275	1	US-08-118-270-66	Sequence 66, Appli
69	318.5	19.6	275	4	PCT-US93-08528-66	Sequence 66, Appli
70	310.5	19.1	269	1	US-08-118-270-64	Sequence 64, Appli
71	310.5	19.1	269	4	PCT-US93-08528-64	Sequence 64, Appli
72	296.5	18.3	331	2	US-09-546-986A-4	Sequence 4, Appli
73	296.5	18.3	331	2	US-09-524-730-4	Sequence 4, Appli
74	291	17.9	322	2	US-09-465-901-34	Sequence 34, Appli
75	285.5	17.6	222	1	US-08-467-948A-27	Sequence 27, Appli
76	285.5	17.6	222	2	US-08-467-947A-27	Sequence 27, Appli
77	283.5	17.1	223	2	US-09-465-901-40	Sequence 40, Appli
78	277.5	17.1	223	2	US-09-465-901-18	Sequence 18, Appli
79	268.5	16.6	223	2	US-09-465-901-26	Sequence 26, Appli
80	268.5	16.6	223	2	US-09-465-901-38	Sequence 38, Appli
81	268	16.5	222	2	US-09-465-901-44	Sequence 44, Appli
82	254.5	15.7	223	2	US-09-465-901-46	Sequence 46, Appli
83	253.5	15.6	223	2	US-09-465-901-16	Sequence 16, Appli
84	252.5	15.6	223	2	US-09-465-901-12	Sequence 12, Appli
85	250	15.4	224	2	US-09-465-901-30	Sequence 30, Appli
86	246.5	15.2	223	2	US-09-465-901-36	Sequence 36, Appli
87	246.5	15.2	223	2	US-09-465-901-42	Sequence 42, Appli
88	245.5	15.1	223	2	US-09-465-901-32	Sequence 32, Appli
89	236.5	14.6	163	3	US-09-680-728-7	Sequence 7, Appli
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91	236.5	14.6	223	2	US-09-465-901-24	Sequence 24, Appli
92	233.5	14.4	223	2	US-09-465-901-14	Sequence 14, Appli
93	231.5	14.3	223	2	US-09-465-901-20	Sequence 20, Appli
94	231.5	14.3	223	2	US-09-465-901-28	Sequence 28, Appli
95	227.5	14.0	223	2	US-09-465-901-22	Sequence 22, Appli
96	215.5	13.3	326	2	US-08-988-876-1	Sequence 1, Appli
97	201	12.4	37	2	US-09-759-143-925	Sequence 95, App
98	201	12.4	37	2	US-10-012-896-925	Sequence 95, App
99	189.5	11.7	177	2	US-08-748-506-21	Sequence 21, Appli
100	189.5	11.7	332	2	US-09-831-206-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-759-143-920
; Sequence 920, Application US/09759143
; Patent No. 6800746
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-920

Query Match      99.8%; Score 1619; DB 2; Length 318;
Best Local Similarity 99.7%; Pred. No. 1e-139;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFLLGLPGLBAQFWLAPLCSLYLAVGNLTIIYVTRHSLHE 60
DB 1 MMVDPNGNESSATYFLLGLPGLBAQFWLAPLCSLYLAVGNLTIIYVTRHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAHSLSGMESTVLLA 120
QY 121 MAPRYYAICHPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAPRYYAICHPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
QY 181 YCHQDVKLACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTVLGLTREAOAKAF 240
DB 181 YCHQDVKLACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTVLGLTREAOAKAF 240
QY 241 GTCVSHCAVFIFVYPIGLSMVHRFSKRSDSPFLVILANIYLLVPVLANPIYVGVTKE 300
DB 241 GTCVSHCAVFIFVYPIGLSMVHRFSKRSDSPFLVILANIYLLVPVLANPIYVGVTKE 300
QY 301 IRRRIILRFHVATHASEP 318
DB 301 IRRRIILRFHVATHASEP 318
```

```
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Basseois, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-920

Query Match      99.8%; Score 1619; DB 2; Length 318;
Best Local Similarity 99.7%; Pred. No. 1e-139;
Matches 317; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVDPNGNESSATYFLLGLPGLBAQFWLAPLCSLYLAVGNLTIIYVTRHSLHE 60
DB 1 MMVDPNGNESSATYFLLGLPGLBAQFWLAPLCSLYLAVGNLTIIYVTRHSLHE 60
QY 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAHSLSGMESTVLLA 120
DB 61 PMYIFLCMLSGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAHSLSGMESTVLLA 120
QY 121 MAPRYYAICHPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
DB 121 MAPRYYAICHPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIISHS 180
QY 181 YCHQDVKLACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTVLGLTREAOAKAF 240
DB 181 YCHQDVKLACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTVLGLTREAOAKAF 240
QY 241 GTCVSHCAVFIFVYPIGLSMVHRFSKRSDSPFLVILANIYLLVPVLANPIYVGVTKE 300
DB 241 GTCVSHCAVFIFVYPIGLSMVHRFSKRSDSPFLVILANIYLLVPVLANPIYVGVTKE 300
QY 301 IRRRIILRFHVATHASEP 318
DB 301 IRRRIILRFHVATHASEP 318
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RESULT 2
US-10-012-896-920
; Sequence 920, Application US/10012896
; Patent No. 6943336
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RESULT 3
US-09-680-728-2
; Sequence 2, Application US/09680728
; Patent No. 6790631
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raltano
```

```
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Douglas C. Saffran
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 129,24US01
; CURRENT APPLICATION NUMBER: US/09/680,728
; PRIOR FILING DATE: 2000-10-05
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-680-728-2

Query Match          99.7%; Score 1617; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSYLIVAVGNLTIIYVTRHSHAP 61
DB 1 MVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSYLIVAVGNLTIIYVTRHSHAP 60
QY 62 MYFLCMLSGDILISTSSMPKMLAIFWFNSTTIQPDACLLQIFAIHSLSGMSTVLLAM 121
DB 61 MYFLCMLSGDILISTSSMPKMLAIFWFNSTTIQPDACLLQIFAIHSLSGMSTVLLAM 120
QY 122 APDRYVAICHLRHATVTLPRVTKIGVAAVRGALMAPLPVFIKQLPFCRSNIISSHY 181
DB 121 APDRYVAICHLRHATVTLPRVTKIGVAAVRGALMAPLPVFIKQLPFCRSNIISSHY 180
QY 182 CLHQDVWKLACDDIRVVVVYGLIVIIISATIGDSLISFSYLLIKTVLGLTREAOAKAFG 241
DB 181 CLHQDVWKLACDDIRVVVVYGLIVIIISATIGDSLISFSYLLIKTVLGLTREAOAKAFG 240
QY 242 TCVSHVCAPFIFFVPPFGLSMVHRFSKRSDPLVILANIYLLVPPVLANPIVGVKTKEI 301
DB 241 TCVSHVCAPFIFFVPPFGLSMVHRFSKRSDPLVILANIYLLVPPVLANPIVGVKTKEI 300
QY 302 RORILRLFHVATNASEP 318
DB 301 RORILRLFHVATNASEP 317

RESULT 4
US-10-017-066A-2
; Sequence 2, Application US/10017066A
; Patent No. 6838258
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Douglas C. Saffran
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 511582002410
; CURRENT APPLICATION NUMBER: US/10/017,066A
; CURRENT FILING DATE: 2002-05-28
; PRIOR FILING DATE: 2000-10-05
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-017-066A-2

Query Match          99.7%; Score 1617; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSYLIVAVGNLTIIYVTRHSHAP 61
DB 1 MVDPNNGESSATYFIIIGLPGLEBAQFWLAFPLCSYLIVAVGNLTIIYVTRHSHAP 60
QY 62 MYFLCMLSGDILISTSSMPKMLAIFWFNSTTIQPDACLLQIFAIHSLSGMSTVLLAM 121
DB 61 MYFLCMLSGDILISTSSMPKMLAIFWFNSTTIQPDACLLQIFAIHSLSGMSTVLLAM 120
QY 122 APDRYVAICHLRHATVTLPRVTKIGVAAVRGALMAPLPVFIKQLPFCRSNIISSHY 181
DB 121 APDRYVAICHLRHATVTLPRVTKIGVAAVRGALMAPLPVFIKQLPFCRSNIISSHY 180
QY 182 CLHQDVWKLACDDIRVVVVYGLIVIIISATIGDSLISFSYLLIKTVLGLTREAOAKAFG 241
DB 181 CLHQDVWKLACDDIRVVVVYGLIVIIISATIGDSLISFSYLLIKTVLGLTREAOAKAFG 240
QY 242 TCVSHVCAPFIFFVPPFGLSMVHRFSKRSDPLVILANIYLLVPPVLANPIVGVKTKEI 301
DB 241 TCVSHVCAPFIFFVPPFGLSMVHRFSKRSDPLVILANIYLLVPPVLANPIVGVKTKEI 300
QY 302 RORILRLFHVATNASEP 318
DB 301 RORILRLFHVATNASEP 317

RESULT 5
US-09-439-313-527
; Sequence 527, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 527
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-439-313-527

Query Match          60.4%; Score 979; DB 2; Length 320;
Best Local Similarity 59.5%; Pred. No. 2.1e-81;
Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;

QY 8 NBSATYFIIIGLPGLEBAQFWLAFPLCSYLIVAVGNLTIIYVTRHSHAPMYFLC 67
DB 5 NHTAT-FVILIGIPGIEKAFHWGFPILSMYVAMFNCIVIVIVTRBSLHAPMYFLC 63
QY 68 MLSGIDILISTSSMPKMLAIFWFNSTTIQPDACLLQIFAIHSLSGMSTVLLAMAFDRY 127
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Db 64 MAAIDALSTSTMPKIALFWPDSREISFBACTQWPFHLSAIBSTILLAMA FDRYV 123
Qy 128 AICHPLEHAATVLTLPRTYKIGVAANVRGALMAMPVPIKOLPFCRSNIISHSYCLHODV 187
Db 124 AICHPLEHAATVLTLPRTYKIGVAANVRGSLFPFPLIKRLAFCHSNVLSHCYHODV 183
Qy 188 MCLACDDIRVVNVVYGLIIVISAIGDSLISFSYLLIKTVLGL-TREAOAKAGTCVSH 246
Db 184 MCLAYADTLERNVYVGLTRAILLVMGVDVWFISLSTFLIRTVLQLPSEBAKAGTCVSH 243
Qy 247 VCAVFIFYPFPIGLSMVHRFSKRDSPLVILANTYLLVPVLPVIVGVYKTEIRORIL 306
Db 244 IGVTLAFYVPLIGLSVHRFGNSLHPYRVVMGDIYLLPVPINPIYGAKTQIRTRVL 303
Qy 307 RLPHVA 312
Db 304 AMFKIS 309

RESULT 6

US-09-636-215-527
Sequence 527, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jlang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kaloos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.4271C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 527
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-215-527

Query Match 60.4%; Score 979; DB 2; Length 320;
Best Local Similarity 59.5%; Pred. No. 2,1e-81;
Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;

Qy 8 NESATYFILIGLPGLEBAQFWLAPPLCSYLLAVLGNLTITTYIVRTEHSLHEPMYFLC 67
Db 5 NPTNAT-FVLIGIGLEKAFHWGFPPLSMYVAMFGNCIVFIVRTERSLHAPMYFLC 63
Qy 68 MLSGIDILISTSSMPKUALFWFNSTTIQPDACILQIFAHISLSGMSSTVLLAMAFDRYV 127
Db 64 MLAADIDALSTSTMPKIALFWPDSREISFBACTQWPFHLSAIBSTILLAMA FDRYV 123
Qy 128 AICHPLEHAATVLTLPRTYKIGVAANVRGALMAMPVPIKOLPFCRSNIISHSYCLHODV 187
Db 124 AICHPLEHAATVLTLPRTYKIGVAANVRGSLFPFPLIKRLAFCHSNVLSHCYHODV 183
Qy 188 MCLACDDIRVVNVVYGLIIVISAIGDSLISFSYLLIKTVLGL-TREAOAKAGTCVSH 246
Db 304 AMFKIS 309

Db 184 MCLAYADTLERNVYVGLTRAILLVMGVDVWFISLSTFLIRTVLQLPSEBAKAGTCVSH 243
Qy 247 VCAVFIFYPFPIGLSMVHRFSKRDSPLVILANTYLLVPVLPVIVGVYKTEIRORIL 306
Db 244 IGVTLAFYVPLIGLSVHRFGNSLHPYRVVMGDIYLLPVPINPIYGAKTQIRTRVL 303
Qy 307 RLPHVA 312
Db 304 AMFKIS 309

RESULT 7

US-09-685-166A-527
Sequence 527, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jlang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kaloos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 527
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-09-685-166A-527

Query Match 60.4%; Score 979; DB 2; Length 320;
Best Local Similarity 59.5%; Pred. No. 2,1e-81;
Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;

Qy 8 NESATYFILIGLPGLEBAQFWLAPPLCSYLLAVLGNLTITTYIVRTEHSLHEPMYFLC 67
Db 5 NPTNAT-FVLIGIGLEKAFHWGFPPLSMYVAMFGNCIVFIVRTERSLHAPMYFLC 63
Qy 68 MLSGIDILISTSSMPKUALFWFNSTTIQPDACILQIFAHISLSGMSSTVLLAMAFDRYV 127
Db 64 MLAADIDALSTSTMPKIALFWPDSREISFBACTQWPFHLSAIBSTILLAMA FDRYV 123
Qy 128 AICHPLEHAATVLTLPRTYKIGVAANVRGALMAMPVPIKOLPFCRSNIISHSYCLHODV 187
Db 124 AICHPLEHAATVLTLPRTYKIGVAANVRGSLFPFPLIKRLAFCHSNVLSHCYHODV 183
Qy 188 MCLACDDIRVVNVVYGLIIVISAIGDSLISFSYLLIKTVLGL-TREAOAKAGTCVSH 246
Db 184 MCLAYADTLERNVYVGLTRAILLVMGVDVWFISLSTFLIRTVLQLPSEBAKAGTCVSH 243
Qy 247 VCAVFIFYPFPIGLSMVHRFSKRDSPLVILANTYLLVPVLPVIVGVYKTEIRORIL 306
Db 244 IGVTLAFYVPLIGLSVHRFGNSLHPYRVVMGDIYLLPVPINPIYGAKTQIRTRVL 303
Qy 307 RLPHVA 312
Db 304 AMFKIS 309


```

: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yaelr A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.42718C18
: CURRENT APPLICATION NUMBER: US/09/651.236
: CURRENT FILING DATE: 2000-08-29
: NUMBER OF SEQ ID NOS: 865
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 527
: LENGTH: 320
: TYPE: FRT
: ORGANISM: Homo sapiens
: US-09-651-236-527

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Query Match	60.4%	Score 979;	DB 2;	Length 320;
Best Local Similarity	59.5%	Pred. No. 2.1e-81;		
Matches 182;	Conservative 55;	Mismatches 67;	Indels 2;	Gaps 2

Cy 0 N E S S A T Y F L I G D P G L E E A Q F M L A F P L C S L Y I L V L G N L I I Y R T E H S L E P E Y I F L C 67
 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
D8 5 N P H T A T - P L L I G I P G L E K A H F W G E P P L S I Y V A A F G N C I V F I Y R T E R S L A A P Y I L F L C 63

Qy	68	M	A	S	G	I	I	I	I	S	T	S	M	P	K	M	A	I	F	E	N	S	T	T	I	Q	E	A	C	I	O	F	A	H	S	I	G	S	E	S	T	I	L	A	M	F	D	R	V	127
Db	64	M	A	I	D	A	L	S	T	S	T	M	P	K	I	L	A	F	E	P	S	R	E	I	S	E	A	C	L	O	M	F	I	H	A	S	I	S	T	I	L	A	M	F	D	R	V	123		

Qy 128 AICHPLRAATVLTPLPRVTIGIGVAIVVRGALMALAPLPVFETKQLPFGRSNITLSSYCLHODY 187

Db 124 AICHPLRAAAVLTNTVTAAIGIGVAIVVRGSLFFFLPPLLKRLAFCSNIVLSSYCVCHODY 183

QY 188 MKLACDDIRVNVVYGLIVIAISAGDLSLSPSYLLILKTVLGL-TREAQAKPCTGVSH 246
Db 184 MKLAVADLTENVVYGLTALLVMGDVMTSLSPFLIRVYLVQLQPSKSERKAFCTGVSH 243

QY 247 VCAVFIFVYFPGISWVHRFSKRSDSPLEPIITANIYLLVPPVLANIVYGVKTKERORIL 306
Db 244 IGVALLAFVYPLIGSVVHRFGNSLHPIVRVWGDVYLLLPVINVPIIYGVAKTKQILRTRL 303

QY	307	RLPHVA	312
	:	:	:
nb	304	AMEKIS	309

RESULT 11
US-09-968-033C-4

```

; Sequence 4, Application US/0956003C
; Patent No. 6824993
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.

```

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1  TITLES OF INVENTION: ADAMIN FIBROBLAST SPECIFIC G-PROTEIN RECEPTOR NFKB1/0
2  FILE REFERENCE: PF180P1
3  CURRENT APPLICATION NUMBER: US/09/968,033C
4  CURRENT FILING DATE: 2001-10-02

```

PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 09/339,115
 PRIOR FILING DATE: 1999-06-24

PRIOR APPLICATION NUMBER: 09/053,303
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 08/465,980
 PRIOR FILING DATE: 1995-06-06

```

: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 4
: LENGTH: 320

```

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: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-968-033C-4

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Query Match	60.4%;	Score 979;	DB 2;	Length 320;
Best Local Similarity	-59.5%;	Pred. No. 2.1e-81;		
Matches 182;	Conservative 55;	Mismatches 67;	Indels 2;	Gaps 2;

8 N E S S A T Y F I L I G P L G L B E A Q F M L A P L C S L Y I A V D G N L T I I Y V R E H S L H E P M Y I F L C 67
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
5 N E T H A T - F V L I G I P G L E K A H F W G P L L S M Y V A M E G N C I V F I V R T E R S L H A P M Y L F L C 63

```
68 MUGSIDIIISTSMFKTALIFWENSTTIQDACLLOIFAHSLSGMESTVLLAMAFDRV 127  
|| : | : | : || : | : | : || : | : | : || : | : | : ||  
64 MAAIDALSTMPKILALFWPDSREISPEACLTQMFPHALSAIESTILLAMAFDRV 123
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128 AICHPELHAATVLTLPRTVKYIGVAAVVRGAALMAPLEVFIKOLPFCRKNILSHSYCHLDGV 187
 ||||| :||:||||| :||:||||| :||:||||| :||:|||||
 124 AICHPELRHAAVLNNTVTQAIGIVAIVRRGSLFFPLPLLKRLAFCHSNVLSSHSCVHQDV 183

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188 MCLACDDIRVNVVYGLIVITSAIGDSLISPSYLLIKTVLGL-TREAQAKAFGTCVSH 246
      ||||| : : : ||||| : : |||||
184 MCLAYADTLPNVVYGLTALLVMGDMVFISLSYFLIRTVQLPSISERAKAFGTCVSH 243

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[illegible]

307 RLEFVA 312
:|::
304 AMFKIS 309
b

RESULT 12
S-09-657-279-527

Sequence 261, application 09/05031215
Patent No. 6894146
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun

APPLICANT: WILSON, DAVIN C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu

APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Panger, Gary R.
APPLICANT: Retter, Marc W.

APPLICANT: stoix, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darick

APPLICANT: Li, Samuel
 APPLICANT: Wang, Aljun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Henler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C19
CURRENT APPLICATION NUMBER: US/09/557,279

CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 877
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 527

LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
-09-657-370-537

Query Match	60.4%	Score 979;	DB 2;	Length 320;
Best Local Similarity	59.5%	Pred. No. 2.1e-81;		
March 1993 Consensus	55.0%	March 1993 Consensus	57.0%	March 1993 Consensus

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8 NSSATVFILIGLPGLEBAQFWLAFLPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYPIC 67
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QY 68 MLAGIDILISTSSMPKMLAIFWPNSTTIOPDACLQIFAIHSLSGMESTVLLAAMPDRYV 127
 DB 64 MLAGIDILISTSSMPKMLAIFWPNSTTIOPDACLQIFAIHSLSGMESTVLLAAMPDRYV 123
 QY 128 AICHPLEHATVLTLPRTKIGVAAVVGAALMAPLPFRIKQLPFCRSNIIISHSYCLHODV 187
 DB 124 AICHPLEHAAVANNVTVAQIGIVAVVAGSLFFPPLPILIRLAFCHSNVLSHSCVHQDV 183
 QY 188 MCLACDDIRVVNVVGLIYVISAIGDLSLISFSYLLIKTVLGL-TREAOKAFGTCVSH 246
 DB 184 MCLAAVDTLPNNVYVGLTALIVMGVDWVFISLSTFPLIRVLDLPKSRERAKAFGTCVSH 243
 QY 247 VCAVFITYVPFGLSWHRSKRRDSPPLYLANIYLLVPPVLANPIYGVYKXIRORIL 306
 DB 244 IGVVLAFTVPLIGLSVHRRGNSLHPYVRVWGDYLLPVPINPIYGAKTQIRTRVL 303
 QY 307 RLPHVA 312
 DB 304 AMFKIS 309

RESULT 13

US-10-012-896-527
 ; Sequence 527, Application us/10012896
 ; Patent No. 6943236
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kelos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Scolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hurrell, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Basbols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Panger, Gary R.
 ; APPLICANT: Mantanabe, Yoshihiro
 ; APPLICANT: Meagher, Madeleine Joy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427C27
 ; CURRENT APPLICATION NUMBER: US/10/012.896
 ; CURRENT FILING DATE: 2001-12-10
 ; NUMBER OF SEQ. ID NOS: 1011
 ; SOFTWARE: FaastSeq for Windows Version 3.0
 ; SEQ ID NO 527
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-012-896-527

Query Match 60.4%; Score 979; DB 2; Length 320;
 Best Local Similarity 59.5%; Pred. No. 2.1e-81;
 Matches 182; Conservative 55; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESAATYPIILIGLPEEAQFWLAFPLCSLYLNAVGNLTITYIVRTEHSLHEPMYIFLC 67
 DB 5 NPTAT-FVLLIGLPEEAQFWLAFPLCSLYLNAVGNLTITYIVRTEHSLHEPMYIFLC 63
 QY 68 MLAGIDILISTSSMPKMLAIFWPNSTTIOPDACLQIFAIHSLSGMESTVLLAAMPDRYV 127
 DB 64 MLAGIDILISTSSMPKMLAIFWPNSTTIOPDACLQIFAIHSLSGMESTVLLAAMPDRYV 123

DB 64 MLAGIDILISTSSMPKMLAIFWPNSTTIOPDACLQIFAIHSLSGMESTVLLAAMPDRYV 123
 QY 128 AICHPLEHATVLTLPRTKIGVAAVVGAALMAPLPFRIKQLPFCRSNIIISHSYCLHODV 187
 DB 124 AICHPLEHAAVANNVTVAQIGIVAVVAGSLFFPPLPILIRLAFCHSNVLSHSCVHQDV 183
 QY 188 MCLACDDIRVVNVVGLIYVISAIGDLSLISFSYLLIKTVLGL-TREAOKAFGTCVSH 246
 DB 184 MCLAAVDTLPNNVYVGLTALIVMGVDWVFISLSTFPLIRVLDLPKSRERAKAFGTCVSH 243
 QY 247 VCAVFITYVPFGLSWHRSKRRDSPPLYLANIYLLVPPVLANPIYGVYKXIRORIL 306
 DB 244 IGVVLAFTVPLIGLSVHRRGNSLHPYVRVWGDYLLPVPINPIYGAKTQIRTRVL 303
 QY 307 RLPHVA 312
 DB 304 AMFKIS 309

RESULT 14

US-09-680-728-3
 ; Sequence 3, Application us/09680728
 ; Patent No. 6790631
 ; GENERAL INFORMATION:
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Aya Jakodovits
 ; APPLICANT: Mary Faris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Steve Chappell Mitchell
 ; APPLICANT: Douglas C. Saffran
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
 ; FILE REFERENCE: 129.24USU1
 ; CURRENT APPLICATION NUMBER: US/09/680.728
 ; CURRENT FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/157.902
 ; PRIOR FILING DATE: 1999-10-05
 ; NUMBER OF SEQ. ID NOS: 50
 ; SOFTWARE: FaastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 320
 ; TYPE: PRT
 ; ORGANISM: Rat Protein
 US-09-680-728-3

Query Match 60.2%; Score 977; DB 2; Length 320;
 Best Local Similarity 59.5%; Pred. No. 3.3e-81;
 Matches 182; Conservative 53; Mismatches 69; Indels 2; Gaps 2;

QY 8 NESAATYPIILIGLPEEAQFWLAFPLCSLYLNAVGNLTITYIVRTEHSLHEPMYIFLC 67
 DB 5 NPTAT-FVLLIGLPEEAQFWLAFPLCSLYLNAVGNLTITYIVRTEHSLHEPMYIFLC 63
 QY 68 MLAGIDILISTSSMPKMLAIFWPNSTTIOPDACLQIFAIHSLSGMESTVLLAAMPDRYV 127
 DB 64 MLAGIDILISTSSMPKMLAIFWPNSTTIOPDACLQIFAIHSLSGMESTVLLAAMPDRYV 123
 QY 128 AICHPLEHATVLTLPRTKIGVAAVVGAALMAPLPFRIKQLPFCRSNIIISHSYCLHODV 187
 DB 124 AICHPLEHAAVANNVTVAQIGIVAVVAGSLFFPPLPILIRLAFCHSNVLSHSCVHQDV 183
 QY 188 MCLACDDIRVVNVVGLIYVISAIGDLSLISFSYLLIKTVLGL-TREAOKAFGTCVSH 246
 DB 184 MCLAAVDTLPNNVYVGLTALIVMGVDWVFISLSTFPLIRVLDLPKSRERAKAFGTCVSH 243
 QY 247 VCAVFITYVPFGLSWHRSKRRDSPPLYLANIYLLVPPVLANPIYGVYKXIRORIL 306
 DB 244 IGVVLAFTVPLIGLSVHRRGNSLHPYVRVWGDYLLPVPINPIYGAKTQIRTRVL 303
 QY 307 RLPHVA 312
 DB 304 AMFKIS 309

RESULT 15
US-10-017-066A-3
Sequence 3, Application US/10017066A
Patent No. 6838258
GENERAL INFORMATION:
APPLICANT: Arthur B. Raitano
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
APPLICANT: Mary Faris
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
TITLE OF INVENTION: UP-REGULATED IN PROSTATE CANCER AND USES THEREOF
FILE REFERENCE: 51158202410
CURRENT APPLICATION NUMBER: US/10/017,066A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: US 09/680,728
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/157,902
PRIOR FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 320
TYPE: PRT
ORGANISM: Rat Protein
US-10-017-066A-3
Query Match
Best Local Similarity 59.5%; Score 977; DB 2; Length 320;
Matches 182; Conservative 53; Mismatches 69; Indels 2; Gaps 2;
QY 8 NEEATYFILGLPGLERAGQWLAFLPGLSLYLAVLGNLTIIYVIRTEHSLHBPYIFLCMLSGIDIL 67
DB 5 NPTNAT-FMLIGIGLEERAHFMFGFPLSMYVAVALFGNCIVFIVTRERSLHAPYIFLCML 63
QY 68 MLSGIDILISTSSMPKMLAIFWNSSTIQFDACLQIFAIHSLSGMSSTVLLMAFDYVAICHPLRH 127
DB 64 MLAIDIALSTMPKMLAIFWNSSTIQFDACLQIFAIHSLSGMSSTVLLMAFDYVAICHPLRH 123
QY 128 AICPLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHODV 187
DB 124 AICPLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHODV 183
QY 188 MCLACDDIRVNVVGLVITISAGLSLISPSYLLIKTVLGL-TREAOKAFGTCVSH 246
DB 184 MCLAVTDLPVNVVGLVITISAGLSLISPSYLLIKTVLGL-TREAOKAFGTCVSH 243
QY 247 VCAVFIPVPPFISGSMVHRFSKRSDPLPVILANITYLVPVLPVIVGVTKERIRL 306
DB 244 IGVALAFVPLIGLSVHRFSGNSLDPVIVLMDGYLLPVPINPIYGAKTKQIRKVL 303
QY 307 RLPHVA 312
DB 304 AMFKIS 309

US-09-968-033C-2
Sequence 2, Application US/09968033C
Patent No. 6824893
GENERAL INFORMATION:
APPLICANT: Soppet et al.
TITLE OF INVENTION: Human Prostate Specific G-Protein Receptor HPPA70
FILE REFERENCE: PFI80B1
CURRENT APPLICATION NUMBER: US/09/968,033C
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,275
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 09/339,115
RESULT 16
US-09-968-033C-2
Sequence 2, Application US/08465980
Patent No. 5756309
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Ruben, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPPA70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,980
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 09/053,303
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 08/465,980
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: SITE
LOCATION: (192)
OTHER INFORMATION: Xaa equals any amino acid
US-09-968-033C-2
Query Match
Best Local Similarity 59.5%; Score 965.5; DB 2; Length 320;
Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;
QY 16 ILIGLPGLERAGQWLAFLPGLSLYLAVLGNLTIIYVIRTEHSLHBPYIFLCMLSGIDIL 75
DB 12 VLIGLPGLERAGQWLAFLPGLSLYLAVLGNLTIIYVIRTEHSLHBPYIFLCMLSGIDIL 71
QY 76 ISTSSMPKMLAIFWNSSTIQFDACLQIFAIHSLSGMSSTVLLMAFDYVAICHPLRH 135
DB 72 LSTSTMPKMLAIFWNSSTIQFDACLQIFAIHSLSGMSSTVLLMAFDYVAICHPLRH 131
QY 136 ATVTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHODV 195
DB 132 AAVLVNNTVIAIGVAVVRGSLPFPPLIKRLAFCHSVNLSHSYCLHODV 191
QY 196 RVNVVGLVITISAGLSLISPSYLLIKTVLGL-TREAOKAFGTCVSHCVAFIF 254
DB 192 XPNVVGLVITISAGLSLISPSYLLIKTVLGL-TREAOKAFGTCVSHCVAFIF 251
QY 255 VPFISGSMVHRFSKRSDPLPVILANITYLVPVLPVIVGVTKERIRL 312
DB 252 VPLIGLSVHRFSGNSLDPVIVLMDGYLLPVPINPIYGAKTKQIRKVL 309
RESULT 17
US-08-465-980-2
Sequence 2, Application US/08465980
Patent No. 5756309
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Ruben, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPPA70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,980
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-339-115-2

Query Match 59.5%; Score 964.5; DB 2; Length 320;
Best Local Similarity 59.4%; Pred. No. 4.5e-80;

Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;

QY 16 ILIGLPGLEAQPWLAPLCSLYLAVLGNLTIIYVTEHSLHBPYIFLCMTSGIDIL 75
DB 12 VLIGPGLEKXHFVWGFPILSMYVAMGNCIVIVTERSLHAPVYLFCLMLAIDLA 71
QY 76 ISTSMPEMLAIFWNSSTTIQPDACLOIPAIHISLGSMESTVLLAMAFDRYVAICHPLRH 135
DB 72 LSTSTMPKILALFWPDSREISIEACTQMPFIHALSAESTILLAMAFDRYVAICHPLRH 131
QY 136 ATVLTLPVTKIGVAAYVGAALMAPLVPFIKQLPFCRSNIISSHSCYCHODVMKLAODDI 195
DB 132 AAVLNTVTQAQIGIVAAVRGSLFFFPPLILKRLAFCHSNVLSHSYCVHODVMKLAAYDT 191
QY 196 RVNVVGLIYIISAIGDSLISFSYLLIKTVLGL-TREAOKAFGTCVSHVCAVPIFY 254
DB 192 LPNVVGLTALLVMGVDMFISLSYFLIIRTVQLPSEKSRKAFGTCVSHIGVLAIFY 251
QY 255 VPFGLSMVHRFSGKRDSPPLVILANIYLLVPPVNPVYGVKTEIRORILRLFHVA 312
DB 252 VPLIGLSVHRFGNSLHPRIVRVWMDIYLLPPVINPIIYGAKTKQIRTRVLAWEFKIS 309

RESULT 20

US-09-680-728-4
Sequence 4, Application US/09680728
Patent No. 6790631

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TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: 129.24USU1
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NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 320
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-680-728-4

Query Match 59.5%; Score 964.5; DB 2; Length 320;
Best Local Similarity 59.4%; Pred. No. 4.5e-80;

Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;

QY 16 ILIGLPGLEAQPWLAPLCSLYLAVLGNLTIIYVTEHSLHBPYIFLCMTSGIDIL 75
DB 12 VLIGPGLEKXHFVWGFPILSMYVAMGNCIVIVTERSLHAPVYLFCLMLAIDLA 71
QY 76 ISTSMPEMLAIFWNSSTTIQPDACLOIPAIHISLGSMESTVLLAMAFDRYVAICHPLRH 135
DB 72 LSTSTMPKILALFWPDSREISIEACTQMPFIHALSAESTILLAMAFDRYVAICHPLRH 131
QY 136 ATVLTLPVTKIGVAAYVGAALMAPLVPFIKQLPFCRSNIISSHSCYCHODVMKLAODDI 195

DB 132 AAVLNTVTQAQIGIVAAVRGSLFFFPPLILKRLAFCHSNVLSHSYCVHODVMKLAAYDT 191
QY 196 RVNVVGLIYIISAIGDSLISFSYLLIKTVLGL-TREAOKAFGTCVSHVCAVPIFY 254
DB 192 LPNVVGLTALLVMGVDMFISLSYFLIIRTVQLPSEKSRKAFGTCVSHIGVLAIFY 251
QY 255 VPFGLSMVHRFSGKRDSPPLVILANIYLLVPPVNPVYGVKTEIRORILRLFHVA 312
DB 252 VPLIGLSVHRFGNSLHPRIVRVWMDIYLLPPVINPIIYGAKTKQIRTRVLAWEFKIS 309

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